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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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11036.050 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. a a O O იი a 221.2 221.2 221.2 221.2 221.2 221.2 220.2 220.2 220.2 220.2 220.2 220.2 217.8 217.8 217.8 217.8 217.8 217.8 217.8 217.8 200 195.2 187.8 185.6 183.2 806.6 806.6 535.4 472.8 4472.8 2442.8 2280.2 232.4 232.4 232.4 232.4 225.6 225.6 225.6 226.6 Score % Query Match 100.0 19.7 18.6 18.1 18.1 18.1 18.1 17.7 17.7 17.0 16.8 0 71177 0 185788 0 219763 0 232119 8 232119 8 244161 7 64328 7 1130 127769 195476 1796 1800 Length 1834 1834 1834 1834 1835 944 1020 1718 1755 1606 1613 1613 1834 DB 10 10 10 10 AX823252 BC0036846 BC0036846 AX676264 AX676269 AF536382 AX335777 AX3353777 AX474697 HUMPROS AC101465 AC101465 AC101465 AC101461 AC093175 AC106629 AC117170 AC106629 AC117170 AC124616 AX375740 AX098193 BC001462 AX098215 AX375744 AC009088 AC135044 BD126485 AX342936 AK075142 AX342934 BD125219 AX480935 BD127529 AX360096 AR256996 Sequence AX375740 Sequence AX335911 Mus muscu BC003851 Mus muscu AB038244 Mus muscu AF378085 Mus muscu AF378085 Mus muscu AF378081 Mus muscu AF362280 Mus muscu AX675583 Sequence AR219285 Sequence BC062334 Homo sapi BC036946 Homo sapi AX676264 Sequence AR256990 Sequence AR256990 Sequence AX335777 Sequence AX335777 Sequence AX336740 Sequence AX43670 Sequence AX474697 Sequence AX474697 Sequence AX474697 Mus muscu AC124461 Mus muscu AC124629 Rattus no AC12417170 Rattus no AC124816 Mus muscu AC124816 Mus muscu AC124816 Mus muscu AC124816 Mus muscu AX512287 Sequence AX512289 Sequence AX360096 Sequence AX480935 Sequence BD127529 Primer fo AC135044 AX098193 BC001462 AX098215 AX375744 AX823252 AX342936 AC009088 AR219284 Sequence AK075142 Homo sapi AX342934 Sequence Description BD126485 Homo sapi Sequence Homo sapi Sequence Sequence Sequence 1 Sequence 9 Primer fo 5 Primer fo Sequence

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX512287	RESULT 1
<pre>Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U.,</pre>	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	Homo sapiens .	Homo sapiens (human)	•	AX512287.1 GI:23392631	AX512287	42.	AX512287 1102 bp DNA linear PAT 27-SEP-2002		

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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A.,
Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A.,
Li,L., Gorman,L., Balinger,S., Scioce,P., Bllerman,R., Malyankar,U.,
Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D.
Proteins and nucleic acids encoding same
Patent: WO 02053/42-A, 45 11-JUL-2002;
Curagen Corporation (US)
Location/Qualifiers
1. 1102
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="utaxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                841 GITTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGGAGCAGGTGATGGGTTCAGAG
                                                                                                                                                                                            961 GCATTCCTGGATTCTGCCAGAATCCTTTTGAGGCCCTTGTCCCATATATCAGTAGGAGTC
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100.0%; Score 1102; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.6e-164;
Matches 1102; Conservative 0; Mismatches 0;
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Rothenberg, M., Stone, D., Boldog, F., Shenoy, S. and Anderson, D. Proteins and mucleic acids encoding same Patent: WO 02053742-A 43 11-JUL-2002; Curagen Corporation (US) Location/Qualifiers 1. 1102 | /organism="Hono sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"
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OY 361 GACGGGGCACACCGGGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG 420 Db 361 GACGGCGCACACCCGCGCAGTGGCGGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG 420	QY 421 GAGCTGGCCCGACCTGCTGCCCTGGCCTGGCCTCACCGCCAGCCTGGGCCCCGCC 480 Db 421 GAGCTGGGCCCGGACCTGCTGCTGCTGGCCTCACCGCCAGCCTGGGCCCAGCCTGGCC	A 81 GTGTGGCCTGTCTGCCCGGGCCTCACACGCTTCGTGCACGCAC	Oy 541 GCCACCGGCTGGGGAGACGTCCAGGAGGAGATCCTCTGCCTCTCCCCTGGGTGCTACAG 600 Db 541 GCCACCGGCTGGGGAGACGTCCAGGAGAGAGAGACTCTCTGCCTCTCCCCTGGGTGCTACAG 600	QY 601 GAAGTGGAGCTGCTGGAGGCAGCTACTAATGTCTCTAAAGCCAGCC	Qy 661 CCCTTCAACTCTCCAGATATTGCCAGGATGCTGTGCTGGCTACCCAGAGGGC 720 Db 661 CCCTTCAACCTCACTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGC 720	Qy 721 CGCAGGGACACCTGCCCAGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCCGC 780 Db 721 CGCAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGAAGGCGGCCGC 780	QY 781 IGGITCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGAGAAAACCGCCCTGGA 840 Db 781 IGGITCCAGGCAGGAAICACCAGCTTTGGGTTTGGCTGTGGAAAACGGCCCTGGA 840	QY 841 GITITCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGCTGATGGGTTCAGAG 900 B41 GITITCACTGCTGTGGCTACCTATGAGGCATGGATACGGAGGCAGGTGATGGGTTCAGAG 900	QY 901 CCTGGGCCTGCCACCACCCAGAAGACCCAGATGATTGTTTACATCAAACG 960 Db 901 CCTGGGCCTGCCTTTCCCACCAGCCCCAGAAGACCCAGTCAGATTGTTTACATCAAACG 960	Qy 961 GCATTCCTGGATTCTGCCAGAATCCTTTTGAGGCCCTTGTCCCATATATCAGTAGGAGTC 1020	QY 1021 TCAACTGGGGCCTAAAAGCCTTGTCCTCCCCTGGGTCTCTCCCACACTCTCTGGGCCTC 1080 Db 1021 TCAACTGGGAACCAAAAGCCTTGTCCTCCCCTGGGTCTCTCTC	QY 1081 TGGGGGTTCTGATGGGGCCTCC 1102 Db 1081 TGGGGGTTCTGATGGGGCCTCC 1102	RESULT 3 AX360096 LOCUS AX360096 2457 bp DNA linear PAT 13-FEB-2002 DEFINITION Sequence 52 from Patent W00200860.	AX360096 AX360096.1 GI:18675722		AUTHORS 1 AUTHORS Charydczak, G. Caenepeel, S. and Charydczak, G. Charydczak, G. TITLE Novel processes JOGENAL Patent: WO 0200860-A 52 03-JAN-2002; Sugen, Inc. (US) FEATURES Location/Qualifiers 1. 2457 /organism="Homo sapiens"

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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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                                  Chordata, Craniata, Vertebrata, Buteleostomi, Primates, Catarrhini, Hominidae, Homo.
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Yue, H., Azimzai, Y., Kallick, D.A., Baughn, M.R., Griffin, J.A., Swarnakar, A., Lal, P.G., Walia, N.K., Hafalia, A.J., Gandhi, A.R., Au-Young, J., Elliott, V.S., Ramkumar, J., Thangavelu, K., Lu, Y., Warren, B.A., Lu, D.A., Lee, E.A., Tribouley, C.M., Arvizu, C., Delegeane, A.M., Yao, M.G., Khan, F.A. and Sanjanwala, M.M. Protein modification and maintenance molecules
Parent: WO 0246383-A 31 13-JUN-2002;
Incyte Genomics, Inc. (US)
Location Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGGACACCTGCCAGGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAGGGGGCCCCTGG
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 2751509CB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 74.0%; Score 815.6; DB 6
Best Local Similarity 99.5%; Pred. No. 3e-119;
Matches 818; Conservative 0; Mismatches 4
   Homo sapiens
Eukaryota, Metazoa,
Mammalia, Eutheria,
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PAT 18-SEP-2002
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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23 TCTAGGGCCATGGCCCGGCACCTCCCCCTTGTGATGCTTGTCATCAGTCCCATC
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PN 7P 202017375-A/2960

PD 22-10AZ-2002

PP 07-JUL-2000 JP 2000253172

PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SH-

PI SHII,

PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,

SHINICHI KOJIMA,

PI TETSUJI OTSUKI, HISASHI KOGA
                                                                                                                                                                                                                                                                                2810 bp DNA linear PAT 1 full-length cDNA and use thereof.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2960 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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                                                                                      945
                                                                                   904 GGGCCTGCCTTTCCCACCCAGAAGACCCAGTCAGAT
                                                                                                                   886 GGGCCTGCCTTTCCCACCCAGCCCCAGAAGACCCAGTCAGAT
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Bconomy, Trade and Industry of Japan, Come Lary-construction: Research Association for Biotechnology; CDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA 5'- & 3'-end one pass sequencing and chone selection: Helix Research Institute (supported by Japan Key Telmology Center etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLQEVELALIGERATCQCLYSQPGFFNLTLQIIPGMLCAGYPEGRDTCGGBSGGFLVC
EGGSRWGOAGTISFGFCGGRRNRPGYFTAVATYBANTROWNGSPPGPAFPTQPCKTQ
SDPQEPRERNCTILPECGRAPREAMPWEAQWWYGGSRPCHGALVSESWYLAPASCT
LDPNSSDSPPRDLDAWRVLLPSRPRARRVARLVQHBNASWDARADLALLQLRTFVNLS
ANARPWCLAFREHYSTPGSRRCRLARRGEPALLGFGALLLEAELLGGRWCHGLYGRGGA
AVAPLPGDPBHALCPAYGKEBFGGGWNGRREPALCGBGTWFLAGIRDFPSGCLRPRA
FPLQTHGPWISHVTRGAYLEDQLAWWGPDGBETETCTCPPPTERPROGGRAPA
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OGGHOVSKLVISIRLPQHLGIRPPLALLELSSRVBESPSALPICLHPAGIPPGASCWV
LGWKEPQDRVPVAAAVSILTGRICDCLYQGILPPGTLCVLYAEGGENRCEMTSAPPLL
CQWTEGSWILVGWAYGSRELFAALGPEEAWISQTVGFANLLPPSGSPHWPTGGSNLC
PPELAKASGSPHAVYFLLLITLLIQS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MTNGTLEPAAEMSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQ
VELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248
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Direct Submission

Submisted (25-MAR-2002) Takao Isogai, Helix Research Institute,

Submitced (25-MAR-2002) Takao Isogai, Helix Research Institute,

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                     Length 670;
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Regulation of human prostasin-like serine protease
                                                                                                                                                                                                                                                                                                                      81; Indels
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Pred. No. 4.9e-65;
0; Mismatches 81
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    670
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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AX342936
Location/Qualifiers
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                                                 CCAGGAGCCTTCCAGGACTCAGCTCTCAGTCCTACCCAGGAAGAACCTGAAGATCTGGAC 142
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TCTGACTCATACTCACTTTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGCCCCCCGTAC 129
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 670)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                     CTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACCATCTGCGGGGGCTCCCTCAT
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Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 1916 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Primer for synthesizing
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JP 2002017375-A/1916.
Homo sapiens (human)
Homo sapiens
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OOE Joint Genome Institute, Stanford Human Genome Center and
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1 (bases 1 to 127769)
DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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Dob Joint Genome Institute.
Dobs Joint Genome Institute.
Submisted (03-AUG-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (Dases 1 to 127769)
Dobs Joint Genome Institute.
Direct Submission
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0
                                                                                                                                          Length 456;
                                                                                                                                                                         Indels
                                                                                                                            Score 442.8; DB 6;
Pred. No. 2.9e-60;
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WO 0198467-A 3 27-DEC-2001;
                                              1. .456
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
              Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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                                                                                                                                          Query Match
Best Local Similarity 98.0%;
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 Patent:
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Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
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                                                                                                                                                                                                                                 Drive, Walnut Creek, CA 94598, USA

On Mar 29, 2003 this sequence version replaced gi:29029216.

On Mar 29, 2003 this sequence version replaced gi:29029216.

Waw.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory

Www-shgc.stanford.edu

Guality: Phrap Quality >=40 99.7% of Sequence;

Estimated Total Number of Errors is 0.2.
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1 (Bases 1 to 1954/6)
DOE Joint Genome Institute.
                                                         Institute, 2800 Mitchell
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                                               Submitted (18-WAR-2003) DOE Joint Genome Institute, 2800 Mitc Drive, Walnut Creek, CA 94598, USA 5 Chases I to 127769) DOE Joint Genome Institute, Stanford Human Genome Center and Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 127769;
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AC135044
AC135044.1 GI:23505535
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
Homo sapiens (human)
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Pred. No. 3.1e-35;
0; Mismatches 3;
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Unpublished
2 (bases 1 to 195476)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /wol_type="genomic_DNA"
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/clone="RP11-388M20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
Alamos National Laboratory
Direct Submission
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Best Local Similarity 98.9%;
Matches 282; Conservative
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408

TITLE JOURNAL AUTHORS

COMMENT

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27404 AGGAATGGGACGCTGGAGCCCGCGGCCCGAGTGGTCGCTGGTGCTGGGCGTGCACTCCCAG 27463
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Identification, assessment, prevention, and therapy of ovarian
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                                                                                                                                                      DB 2; Length 195476;
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0; Mismatches 401; Indels
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                                                                                                                                                                                      3; Indels
                                                                                 /clone="CTD-2551B20"
/clone_lib="CalTech human BAC library D"
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Millennium Predictive Medicine, Inc. (US)
Location/Qualifiers
                                                                                                                                                    Score 280.2; DB 2, Pred. No. 2.8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                       0; Mismatches
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Sequence 105 from Patent W00118542.
             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                               chromosome="16"
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                                                                                                                                                      25.4%;
98.9%;
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Matches 282; Conserv
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Consensus quality: 180538 bases at least Q30
Consensus quality: 180958 bases at least Q30
Consensus quality: 180958 bases at least Q30
Consensus quality: 180958 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarosse-fp estimation
Quality coverage: 6.7 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft" sequence. It currently
* consists of 22 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
             Direct Submission
Submitted (05-OCT-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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contig of 12483 bp in length
gap of unknown length
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contig of 1993 b
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contig of 2490 b
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contig of 4192 b
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contig of 4872 b
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                                                                  -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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 Joint Genome Institute
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FEATURES

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Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McMann, P.J., Neckennan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Norley, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Murny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y. Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, D., Wutterfield, Y.S., Krzywinski, M.I., Skalska, U., Samitz, J., Myers, R.M., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and
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/protein_id="AaH01462.1"
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ITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKEAYEVKLGA
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighl,P.,
Hansen,N., Ho,S.L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Matrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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Series: IRAL Plate: 4 Row: j Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 21536453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nstitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: ATCC Rubin Laboratory CDM Library Preparation: Rubin Laboratory CDM Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing Dy: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12655206
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/clone lib="NIH_MGC_21"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
/clone="MGC:2133 IMAGE:3138532"
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'note="synonym: PROSTASIN"
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Web site: http://www.nisc.nih.gov/
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Contact: MGC help desk
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1 (Bases I to 180)

2 (Rases I to 180)

3 trausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Strausberg, R.L., Sehmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heiseh, F., Staplethenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Search completed: February 25, 2004, 10:31:04 Job time: 4339 secs

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Description	Abq93901 Hum	Abg93902 Human pro			Aak94500 Human ful	Human	Human		• •	Aas69040 DNA encod	Aaf98698 Human ova	Aaf98720 Human lat	Human	Abt31936 Human bre			Abq86176 Novel hum	Abs67730 DNA encod	Aas01360 Human ser	Abs76501 cDNA enco	σ	68512	Abl68248 Kidney ca	
ΩI	ABO9	ABQ93902	ABK31795	ABQ75956	AAK94500	ABK13565	AAK92190	AAK93456	ABK13566	AAS69040	AAF98698	AAF98720	ABZ35336	ABT31936	ABA94396	ABQ86175	ABQ86176	ABS67730	AAS01360	ABS76501	ABL67949	ABL68512	ABL68248	
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24 221.2 20.1 1834 6 ABK12241 25 221.2 20.1 1834 6 ABN95716 26 220.6 20.0 1668 3 AAC7814 28 205.2 18.6 786 6 ABA94394 29 205.2 18.6 786 6 ABA94394 30 195.2 18.6 2122 5 AAS70551 31 185.6 16.8 882 6 ABN85395 32 183.2 16.6 1142 3 AAC87795 34 183.2 16.6 1142 4 AAF55268 35 183.2 16.6 1142 4 AAF55268 36 183.2 16.6 1169 3 AAC87795 37 180.8 16.4 768 4 AAF55267 38 176.2 16.0 1327 3 AAC8237 41 176.2 16.0 1327 3 AAC82367 42 176.2 16.0 1327 7 ACA63602 44 176.2 16.0 1327 7 ACA63602 44 176.2 16.0 1327 7 ACA63602 44 176.2 16.0 1327 7 ACA63602	Abk12241 cDNA enco Abn95716 Gene #221	Aac77814 Human can	Aas01366 Recombina	Aba94394 Human pro	Aas74051 DNA encod	Abs56430 Mouse cha	Abn85394 Partial H	Abn85395 Partial H	Aac87796 Activatio	Aaf55268 Nucleotid	Aac87795 Activatio	Aaf55267 Nucleotid	Aah78206 Nucleotid	Abn85393 Human NOV	Aaz34034 Human EST	Aac78495 Human EST	Aac58237 Human EST	Acd42567 Novel hum	Aca63602 Novel hum	Aca71766 Human sec	Abx92406 Human PRO
221.2 20.1 1834 220.6 20.0 1688 216.8 20.0 1688 205.2 18.6 786 205.2 18.6 786 195.2 18.6 2122 185.6 16.8 82 183.2 16.6 1142 183.2 16.6 1169 183.2 16.6 1169 183.2 16.6 1169 183.2 16.0 1169 176.2 16.0 1327 176.2 16.0 1327 176.2 16.0 1327 176.2 16.0 1327 176.2 16.0 1327 176.2 16.0 1327	ABK12241 ABN95716	AAC77814	AAS01366	ABA94394	AAS74051	ABS56430	ABN85394	ABN85395	AAC87796	AAF55268	AAC87795	AAF55267	AAH78206	ABN85393	AAZ34034	AAC78495	AAC58237	ACD42567	ACA63602	ACA71766	ABX92406
221.2 20.1 221.2 20.1 226.6 20.0 216.8 19.7 205.2 18.6 195.2 18.6 198.5 16.8 183.2 16.6 183.2 16.6 183.2 16.6 183.2 16.6 183.2 16.6 180.8 16.0 176.2 16.0 176.2 16.0 176.2 16.0 176.2 16.0	ψψ	m	4	9	Ŋ	7	9	9	m	4	m	4	4	9	0	ო	٣	7	7	7	7
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	20.1	20.0	19.7	18.6	18.6	17.7	16.8	16.7	16.6	16.6	16.6	16.6	16.4	16.2	16.0	16.0	16.0	16.0	16.0	16.0	16.0
4 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	221.2	220.6	216.8	205.2	205.2	195.2	185.6	184	183.2	183.2	183.2	183.2	180.8	179	176.2	176.2	176.2	176.2	176.2	176.2	176.2
	24 7.7	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

ABQ93901 standard; DNA; 1102 BP.

RESULT 1

ABQ93901

(first entry)

01-NOV-2002

ABQ93901;

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Human, NOVX; neurological disorder; Alzheimer's disease;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;

KW addiction; tuberous sclarosis; cancer; immune disorder; allergy;

KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

KW endometriosis; incontinence; psoriasis; soleroderma; alopecia;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

KW metabolic pathway regulation disorder; cytostatic; neuroprotective;

M metabolic pathway regulation disorder; cytostatic; neuroprotective;

KW dermatological; antibacterial; antiarthritic; heparotropic; neurogenesis;

KW dermatological; antibacterial; antiarthritic; heparotropic; neurogenesis;

KW dermatological; proliferation; motility; haematopoiesis; wound healing;

KW anglogenesis; forensic biology; transgenic animal; drug screening;

KW gene therapy; NOVL4a; prostatin precursor-like; chromosome 16; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Product= "NOV14a"
note= "No stop codon given in the specification"
                                                                                          Human prostatin precursor-like NOV14a DNA, SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "NOV14a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-2001; 2001US-0260018P.
08-JAN-2001; 2001US-0260360P.
28-FEB-2001; 2001US-0272411P.
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19. .1050
/*tag= b
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5'UTR
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Claim 9a; Page 142; 323pp; English
02-MAR-2001; 2001US-0272817P.
05-JUL-2001; 2001US-0303231P.
12-JUL-2001; 2001US-0305060P.
10-SEP-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318700P.
04-JAN-2002; 2002US-00037417.
                                                                                                                                                                                                                                                                                                                       LOO.0%;
Best Local Similarity 100.0%;
Matches 1102; Conservative 0:
                                    (CURA-) CURAGEN CORP
                                                                             WPI; 2002-583619/62
P-PSDB; ABB09523.
                                                        Gorman L, Edi
Rothenberg M,
                                                   Patturajan M,
                                                                   Padigaru M,
                                                         Gorman
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Tresagecedecedecesagregreegracrecressecrecaecaecaecaecere 360
CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAG 180
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                                                                                                                                                                                                                                                                                                                                                                 241 TCCCTCATCGCCCCCTCCTGGGTCCTCTCCCCTGCTCTTTCATGACGAATGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 GAGCTGGGCGCGGACCTGGCCCTGCCCTGGCCTCACCCGCCAGCCTGGGCCCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAGGCGGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 GACGGCGCACACCCCCCCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 GAGCTGGGCGCCGACCTGGCCCGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCC
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                                           CCCCCGTACTGCGGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAG
                                                                                                                                                                                      TCCCTCATCGCCCCCCCCCGGGGCCTCCCCGCTGCTCACGTTTCATGACGAATGGGACG
                                                                                                                                               CCGGGCACCTGGCCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (AB093879-AB03902). NOVX proteins and connected acids encoding them (AB093879-AB03902). NOVX proteins and connected disorders or in the manufacture of a medicament for treating such disorders with specific applications described for each of the 24 sociated disorders or their homology to known proteins. Various disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tubercous sclerosis, cancers (e.g., alpregies and autoimmune diseases), wyssthenia gravis, asthma, carious forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endomerriosis, carrious forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endomerriosis, cirrhosis, glomerular endothalosis, polycystic kidney disease, endocring cirrhosis, glomerular endothalosis, polycystic kidney disease, endocring disorders, obesity, bacterial infections and particularly cardiomyopathy. CC disorders, obesity, bacterial infections and particularly cardiomyopathy contents of identify cellular receptors or downstream effectors which the used to identify cellular receptors or downstream effectors which can energenesis, cell differentiation, cell motility, cellular cardiomeral molecules that useful and source of primers or probes for forests byte and comprising NOVX mucleic acids such cidentify and cloning NOVX homologues in other cell types. Cell dentifying and cloning NOVX homologues in other cell types. Cell dentifying and cloning NOVX are useful for redensing non-human cransing precurses and electronic properting and cloning not redensity of NOVX activity. The present sequence represents by encoding the correction and coloning not connected to the present sequence represen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 descectificates descentes exercises en estados en en estados en en estados en estados en entre en
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                                                                                                                                                                                                                                                                                                                                         Alsobrook JP, Tchernev VT, Liu X, Spytek KA;
M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM,
Edinger S, Sciore P, Ellerman K, Malyankar U;
M, Stone D, Boldog F, Guo X, Shenoy S, Anderson
, Taupier RJ, Miller CE, Eisen A;
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; Pred. No. 8.2e-185;
0; Mismatches 0;
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1080

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ABQ93902 standard; DNA; 1102

ABQ93902 ID ABQ9 XX

GTGGCCAATTCTGACTCATACTCACTTTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGC 120

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840 900 900 960

780 780 840

480 480 540 540 009 900 99 099 720 720

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(first entry) 01-NOV-2002

Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45.

Human, NOVX; neurological disorder; Alzheimer's disease;

Huntington's disease; Parkinson's disease; pain; behavioural disorder;

Huntington's disease; Sclerois; cancer; immune disorder; allergy;

addiction; tuberous sclerois; cancer; immune disorder; allergy;

Why addiction; cardiovascular disease; hypertension; reproductive disorder;

Hyproiditis; cardiovascular disease; hypertension; reproductive disorder;

Hypertensitis; cirrhosis; glomerular endotheliosis; bacterial infection;

My pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

My pancreatitis; cirrhosis; endocrine disorder; obesity; cardiomyopathy;

My pancreatitis; cirrhosis; endocrine disorder; obesity; cardiomyopathy;

My etheroslerosis; cell signal processing-related disorder;

My metabolic pathway regulation disorder; cytostatic; neuroperotective;

antiniflammatory; immunosuppressive; analgesic; antiatherosclerotic;

dermatological; antibacterial; antiarthritic; heparotropic; neurogenesis;

differentiation; proliferation; motility; heparotropic; neurogenesis;

angiogenesis; forensic biology; transgenic animal; drug screening;

my gene therapy; NOV14b; prostatin precursor-like; gene; ds.

Home sapiens

Location/Qualifiers 1. .18 /*tag= b /product= "NOV14b" 1093. .1102 /*tag= c /*tag= a 19. .1092 Key 5'UTR CDS

WO200253742-A2

11-JUL-2002

07-JAN-2002; 2002WO-US000375

08-JAN-2001; 2001US-0260360P. 28-FEB-2001; 2001US-0272411P. 02-MAR-2001; 2001US-0272411P. 05-JUL-2001; 2001US-0303231P. 12-JUL-2001; 2001US-0318405P. 12-SEP-2001; 2001US-0318406P. 2002US-00037417 04-JAN-2002; 05-JAN-2001;

(CURA-) CURAGEN CORP

ï Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA; Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U; Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson Padigaru M, Taupier RJ, Miller CE, Eisen A; Padigaru M,

WPI; 2002-583619/62.

P-PSDB; ABB09524

receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders. Novel polypeptides and nucleic acids homologous to transmembrane

Claim 9a; Page 143; 323pp; English.

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24

CC disorders are associated with NOVX proteins including neurological disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., colorectal cancer, leukaemia and osteosarcoma), immune diseases (e.g., nallergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, pancreaticis, incontinence, psoriasis, scleroderma, alopecia, ulcers, pancreaticis, cirrhosis, gobesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NoVX nucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which binds to a NOVX protein, and are also useful as targets for the constinction, haematopoiesis, wound healing and angiogenesis. NoVX nucleic acid sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NOVX homologues in other cell types. Cells comprising NOVX nucleic acids are useful for studying the function and critity of NOVX proceins and for identifying and evaluating modulators of NOVX accinity. The present sequence represents DNA encoding the ó 480 Greeccaarrereacrearacreacrracegrirecreecerecesacces CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAG 180 CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAG 180 TCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCATGTTCATGACGAATGGGACG 300 360 420 GACGGCGCGCACACCCCGCCAGTGGCCGCCATCGTGCTGCCGGCCAACTACAGCCAAGTG 420 480 GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG 600 900 9 1 GGGCCCTTGTCCTGGGCCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGGCCTGGGGGCT 1 deseccinérecreseceareseceasandes de la sesection de la seconda de la s GIGGCCAATICIGACICAIACICACITIACGGGIIGGIGCCGICCGGACCCGCIAGGGGC COGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC CCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC TTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCTG GAGCTGGGCCCTGCCTGCTGCGCCTCGCCTCACCCGCCAGCCTGGGCCCCGCC GTGTGGCCTGTCTGCCCCCCCCCCCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGG grereccrercreccreccececercacacacecricerecacacacacacecrecres GCCACCGGCTGGGGAGACGTCCAGGAGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG Gaps 0 Length 1102; Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other; Indels 100.0%; Score 1102; DB 6; 100.0%; Pred. No. 8.2e-185; tive 0; Mismatches 0; prostatin precursor-like protein NOV14b Matches 1102; Conservative Local Similarity 19 19 121 181 181 241 361 421 481 541 121 241 301 301 361 421 481 Query Match g à qq à à g à 음 셤 à 셤 ð 임 à g à 요 à

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                 GAAGTGGAGCTAAGGCTGCTGGGGGGGCCACCTGTCAATGTCTCTACAGGCCAGCCGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         novel human protease #52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocular disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding
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The present invention relates to the isolation of novel human proteases,
and the mucleic acids encoding them. The sequences of the invention are
conditionally immune-related diseases and disorders (e.g. breast,
colon, lung), immune-related diseases and disorders (e.g. inflammatory
diseases and asthma), cardiovascular diseases (e.g. restenosis and
coronary thrombosis), brain or neuronal-associated diseases, metabolic
disorders (e.g. diabetes, obesity), inflammatory disorders (e.g.
cronary thrombosis), prain or neuronal-associated diseases, metabolic
disorders (e.g. diabetes, pain, sexual dysfunction, mood disorders, attention
diseases, migraines, pain, sexual dysfunction, mood disorders, attention
disease, and disorders (e.g. Alzheimer's disease, Parkinson's
disease) and dyskinesias. The nucleic acids and polypeptides are also
useful for treating viral infections such as ocular disease (e.g.
disucoma) and macular degeneration. ABX31802 represent DNA
sequences encoding for the novel human proteases of the invention
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treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
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Pred. No. 1.6e-134;
0; Mismatches 4;
                                                                                                   Claim 26; Fig 18S-TT; 313pp; English.
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Best Local Similarity 99.5
Matches 818; Conservative
                                                         disorders.
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766 Trccasgeasquaccasgerrrescrrrescrrrescreresacesasaacceccresasrr 825 TTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 903 TTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCT 885

844 826 904

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GGGCCTGCCTTTCCCACCCCAGAAGACCCCAGTCAGAT 927 GGGCCTGCCTTTCCCACCCCAGCCCCAGAGACCCCAGTCAGAT

RESULT 4

TTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGAGTT

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ABQ75956 standard; cDNA; 2681 BP
                                                                                                        17-OCT-2002 (first entry)
ABQ75956
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Human; PMWM; protein modification and maintenance molecule;
anticonvulsant; neuroprotective; nootropic; cytostatic; antipsoriatic;
anticonvulsant; neuroprotective; nootropic; cytostatic; antipsoriatic;
anticonvulsant; antiinflammatory; anticonflam, anticonflam;
anticonflammatory; anticulcer; anticonflam, cardiant;
hepatotropic; osteopathic; anticulcer; anticonflamrheic; laxative;
anticonflammatory; anticonflammatory; anticocollar; vasotropic;
anticonflammator; anti-HIV; thrombolytic; anticocollar; anticocollar; anticocollar; anticocollar; immunosuppressive; anticollar;
antitumour; antirheumatic; immunosuppressive; antiallergic; antithyroid;
nephrotropic; antigout; thyromimetic; antiarthritic; uropathic;
ophthalmological; antidepressant; neuroleptic; antinfertility;
anditory; antiseborrheic; antidepressant; neuroleptic; antinfertility;
anticommunicatic colliproliferative; developmental; epithelial;
scables; neurological; Alzheimer's disease; reproductive;
ectopic pregnancy; gene therapy; vaccine; disorder; prostasin; gene; ss. Human PMMM encoding sequence Incyte ID 2751509CB1.

/product= "protein modification and maintenance molecule" location/Qualifiers ø 1. .2457 /*tag= a

WO200246383-A2

13-JUN-2002

05-DEC-2001; 2001WO-US046964

08-DEC-2000; 2000US-0254399P. 21-DEC-2000; 2000US-0257803F. 05-JAN-2001; 2001US-0260110P. 19-JAN-2001; 2001US-0264629P. 25-JAN-2001; 2001US-0264623P.

(INCY-) INCYTE GENOMICS INC.

Swarnakar A; Elliott VS; Griffin JA, Swarnak, Au-Young J, Elliot A, Lu DAM, Lee EA; o MG, Khan FA; Yue H, Azimzai Y, Kallick DA, Baughn MR, Grii Lal PG, Walia NK, Hafalia AJA, Gandhi AR, Au Ramkumar J, Thangavelu K, Iu Y, Warren BA, In Tribouley CM, Arvizu C, Delegeane AM, Yao MG,

WPI; 2002-519664/55. P-PSDB; ABB98135 New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.

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The invention relates to an isolated Protein Modification and Maintenance diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. bypetreision), autoimmune/inflammatory disorders (e.g. anaemia), cell proliferative disorders, developmental disorders (e.g. anaemia), cell proliferative disorders, developmental disorders, epithelial disorders reproductive disorders (e.g. ectopic prepancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the effects of exogenous compound on the expression of nucleic acid and amino acid sequence of protein modification and maintenance molecules. The current sequence represents a human PMMM encoding sequence of the invention, encoding a polypeptide which has been found to have homology
Claim 5; Page 196; 200pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with rat prostasin
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Sequence 2681 BP; 431 A; 919 C; 861 G; 470 T; 0 U; 0 Other;

ö 243 CCGIACIIGCGGGCGCCTGAGCCCTCGGCCCCGCAICGTGGGGGGCTCAAACGCGCGCAGCCG CTGGACTGCGGGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGGCTCAAACGCGCAGCCG 184 GGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCC Gaps Query Match

74.0%; Score 815.6; DB 6; Length 2681;
Best Local Similarity 99.5%; Pred. No. 1.6e-134;
Matches 818; Conservative 0; Mismatches 4; Indels 0; 124 106 셤 à

303 crearesecerecressicerereserecresererererererereses GECACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGCTCC CTCATCGCCCCCCCCCCGCTCCTCCCGCTGCTCACTGTTCATGACGAATGGGACGTTG GAGCCCGCGGCCGAGTGGTCGCTACTGCTGGCGCGTGCACTCCCAGGACGGGCCCCTGGAC 226 (166 244 304

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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; viucide; osteopathic; antiinflammatczy; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPP; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; denstmann-Straussler Syndrome; viral infection; Scrapie;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 TCTGACTCATACTCACTTTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGCCCCCCCGTAC 129
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Pred. No. 6.2e-133;
0; Mismatches 74;
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(1 Similarity 92.0%;
862; Conservative
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P-PSDB; AAU75082 Xiao Y, Key

Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss.

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Homo sapiens

Location/Qualifiers complement (3. .536)

note= "No start or stop codons shown" *tag= a product= "Prostasin-like enzyme" partial

WO200198467-A2

27-DEC-2001

22-JUN-2001; 2001WO-EP007117.

23-JUN-2000; 2000US-0213588P. 20-MAR-2001; 2001US-0276909P.

(FARB) BAYER AG.

Morozov V;

WPI; 2002-114576/15.

Novel human prostasin-like serine protease polypeptide and polymucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.

Claim 1; Fig 1; 111pp; English

This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for requlating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease and reagents and methods specific the human prostasin-like serine protease is useful for immunodetection and for prostasin-like serine protease is useful for immunodetection and inpay specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atheroselserosis, ineurodegenerative disease (C. g. prion protein amyloid plaques of Genstmann-Strausslers Syndrome, Centzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease enterpeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine procease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences prostasin-like serine protease #1 nucleotide sequence of the invention which encode the enzyme. The present sequence represents the human

Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other;

.; 0 Gaps .; 0 Score 535.4; DB 6; Length 537; Pred. No. 3e-85;); Mismatches 1; Indels 0 .; 0 48.68; 99.88; Query Match Best Local Similarity 99.8 Matches 536; Conservative

302

GGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGCGTGCACTCCCCAGGACGGGCCCCTGGA 362 303

CCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGCT 478

CCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTT

243 537

ð g à

AAK92190 standard; cDNA; 670 (first entry) 06-NOV-2001 AAK92190; AAK92190 RESULT

Human cDNA 5'-end sequence, SEQ ID NO: 650

Human; full length cDNA; cDNA synthesis; oligo-capping;

Homo sapiens

EP1130094-A2

05-SEP-2001.

07-JUL-2000; 2000EP-00114089.

08-JUL-1999; 99JP-00194486. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765.

(HELI-) HELIX RES INST

Η; Ishii S, Kawai Y; S, Otsuki T, Koga Hayashi K, K, Kojima kawa T, Isogai T, Sugiyama T, Nagai Nishikawa T, Wakamatsu A, Ota T,

WPI; 2001-524255/58.

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.

SEQ ID NO 650; 1380pp + Sequence Listing; English. Claim 2;

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for claritying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA.

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libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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Best Local Similarity 86.9%; Pred. No. 2.9e-74;
Matches 563; Conservative 0; Mismatches 81; Indels 4
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were burntion of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from

830 Primers useful for synthesizing full length cDNA clones and their

in genetic manipulation.

WPI; 2001-524255/58

Wakamatsu A,

Ē,

Example 11; SEQ ID NO 1916; 1380pp + Sequence Listing; English.

H;

Kawai Y; T, Koga

Otsuki Ishii S,

Nishikawa T, Isogai T, Hayashi K, Is su A, Sugiyama T, Nagai K, Kojima S,

07-JUL-2000; 2000EP-00114089.

05-SEP-2001

99JP-00194486

08-JUL-1999;

11-JAN-2000; 2000JP-00118774 02-MAY-2000; 2000JP-00183765

(HELI-) HELIX RES INST

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Human; full length cDNA; cDNA synthesis; oligo-capping;

EP1130094-A2 sapiens

Ното

Human cDNA clone representative sequence,

(first entry)

06-NOV-2001

AAK93456;

BP

AAK93456 standard; cDNA; 670

RESULT 8

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188

248 202

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prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease purified from human seminal fluid. An antibody specific from human seminal fluid. An antibody specific diagnosis of micro-meteastases, auch susful for immundetection and diagnosis of micro-meteastases, auch as useful for immundetection and diagnosis of micro-meteastases, auch as metastasis of medignate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease (CoPD) protein amyloid plaques of Genstmann-Straussler Syndrome, creuzfeldt-Jakob disease, Scrapie, or infection, particularly viral infection. The human prostasin-like serine protease gene provides a therapeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the uncleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; attenosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genetralende-Jakob disease; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; ligid accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
    548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention comprises the cDNA and protein sequences of an isolated
                                                                                                                                    CTGGGGAGACNTCCANGGAGGCAAATTCTCTGCCTCTCCCCTGGGTGCTACAAGGAAGTG
TGTCTGCCTGCCCGCGCCTCACCGCTTCGTGCACGGCACCGCCTGCGCCACCGG
                                            TGTCTGCCTGCCCCGCGCCTCACACGCTTCGTGCACGGCACCGCCTGCTGCGCCACCG
                                                                                         CTGGGGAGACGTCCA-GGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTAC-AGGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoporosis; Paget's disease; ss; EST; expressed sequence tag.
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                                                                                                                                                                                 GAGCTAAGGCTGCTGGGCG-AGGCCACCTGTCAATGTCTCTACAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostasin-like serine protease cDNA #2
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20-MAR-2001; 2001US-0276909P.
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osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #2 nucleotide sequence of the invention
                                                                                                                                                                                                                                                                                CCCGCGGCCGAGTGGTCGGTACTGTGGGCGNTGCACTCCAAGGACGGCCCTGGACGGC
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                                                                                                                                                                                         Score 442.8; DB 6; Length 456;
Pred. No. 5.6e-69;
0; Mismatches 9; Indels 0;
                                                                                                                                                             Sequence 456 BP; 74 A; 151 C; 167 G; 62 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #4844.
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98.0%;
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2000US-00649167.
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                                                                                                                                                                                                                            447; Conservative
                                                                                                                                                                                                           Local Similarity
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23-AUG-2000;
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AAF98698 standard; DNA; 1796 BP AAF98698; RESULT 11 d ð 셤 ò g à The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to traed disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of dara and products dependent on DNA and am to produce other types of data and products dependent on DNA and and a cold sequences. AAS64157-AAS94564 represent novel human diagnostic 240 300 651 711 351 411 531 GTGCTACAGGAAGTGGAGCTAAGGCTGCTGGGCCAGGCCACCTGTCAATGTCTCTACAGC 360 361 CAGCCCGGTCCCTTCAACCTCACTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTAC 420 471 coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at GCCTGCTGGGCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTCCCTCTCCCCTGG 293 ATGGGACGTTGGAGCCCGCGCCCGAGTGGTCGGTACTGCTGGGGGCGTGC-ACTCCCAGGAC 61 GGGCCCCTGGACGGCGCGCACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTAC 121 AGCCAAGTGGAGCTGGGCGCGACCTGGCCTGCTGCGCCTGGCCTCACCGGCCAGCCTG GGCCCCGCCGTGTGGCCTGTCTGCCTGCCCCGCGCCTCACACGCTTCGTGCACGGCACC GCCTGCTGGGCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGG GTGCTACAGGAAGTGGAGCTAAGGCTGCTGGGCGAGGCCACCTGTCAATGTCTCTACAGC CAGCCCGGTCCCTTCAACCTCACTCTCCAGATATTGCCAGGGATGCTGTGTGCTGGCTAC Arideda de cueda e de consecuencia de consecue GGCCCCGCCGTGTGGCCTGTCTGCCTGCCCCGCGCTTCACACCGCTTCGTGCACGGCACC GGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCCAACTAC Gaps New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity. 1; 39.3%; Score 433.4; DB 5; Length 597; 99.6%; Pred. No. 2.5e-67; ive 0; Mismatches 1; Indels 1; Sequence 597 BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other; 712 CCAGAGGGCCGCAGGGACACCTGCCAG 738 421 CCAGAGGCCGCAGGGACACCTGCCAG 447 electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences Claim 1; SEQ ID NO 4844; 103pp; English Tang YT; Matches 445; Conservative Drmanac RT, Liu C, WPI; 2001-639362/73 Local Similarity (HYSE-) HYSEQ INC P-PSDB; ABG04853

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is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see ARP98954 to AAP98730), in a patient sample, and (2) the normal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybriddoms, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
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                                                                                                                                                                                                                                                                                                                                                                     Human, ovarian cancer, identification, detection, characterisation, tumour, kinase, marker, cytostatic, antisense gene therapy, ds.
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21.1%; Score 232.4; DB 5; Length 1796;
Best Local Similarity 55.0%; Pred. No. 4.8e-32;
Matches 508; Conservative 0; Mismatches 401; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1796 BP; 327 A; 599 C; 511 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                      Human ovarian cancer cell expressed sequence 10798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1001-1002; 1198pp; English.
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16-MAR-2000; 2000US-0190347P.
21-MAR-2000; 2000US-0191321P.
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20-JUL-2000; 2000US-00220467.
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                                                                                                                                                                                                        (first entry)
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AAF99698

AAF99698

AAF99698

AAF9

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of ovarian cancer, of a variety of markers.

Lillie J;

Thompsho P,

2000US-00220467

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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see ARPS9824 to ARP98330), in a patient sample; and (2) the normal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (1) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated for: (3) inhibiting ovarian cancer in a patient. ARF98573 to ARF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
                                                                                                                                                                                                                                           Detection, assessment, prevention and therapy comprises detecting changes in the expression
                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                         Claim 1; Page 1186-1187; 1198pp; English
  03-SEP-1999; 99US-0152547P.
16-MAR-2000; 2000US-0190347P.
21-MAR-2000; 2000US-019131B.
31-MAY-2000; 2000US-0208382P.
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                                                                                 20-JUL-2000;
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Human, ovarian cancer, identification, detection, characterisation, tumour, kinase, marker, cytostatic, antisense gene therapy; ds.

01-SEP-2000; 2000WO-US024199

15-MAR-2001

Homo

Human late stage ovarian tumour polynucleotide marker 28

(first entry)

02-JUL-2001

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                     <u> GTCACTGGCTGGGGTCATGTGGCCCCCTCAGTGAGCCTCCTGACGCCCAAGCCAAGCCACTGCAG</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene expression profile polynucleotide SEQ ID NO 447.
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                                                                                                                                                                                                                                                                                                                                                                  1037 GTGTACACTCTGGCCTCCAGCTATGCCTCCTGGATCCAAAGCAAGGTGACAGAACTCCAG 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the use of specific DNA markers. The method of the invention is useful in the detection and treatment of ovarian and breast cancer. DNA sequences ABT31894 - ABT31949 encode human breast/ovarian cancer-related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCCAGCTGGGGGCT 140
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                                                                                                                          TGGTTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer / ovarian cancer related coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1733 BP; 311 A; 578 C; 500 G; 344 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; breast cancer; ovarian cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1097 ccrcargregreccccaaacccas 1120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   924
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGGGCCTGCCTTTCCCACCCAG
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2001US-0301351P.
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Best Local Similarity 54.9
Matches 507; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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"prostasin-like serine protease"

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22-JUN-2001; 2001WO-EP007116.
                          23-JUN-2000; 2000US-0213474P.
22-MAR-2001; 2001US-0277612F.
                                                2002-114575/15
                                                   P-PSDB; ABB07286
                                    (FARB ) BAYER AG
        WO200198466-A2
              27-DEC-2001
                                          Xiao Y;
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The invention relates to human prostasin-like enzyme polypeptides and polynucleotides. The enzyme can be expressed by standard recombinant methodology. The polypeptide, polynucleotide and modulators are useful cor treating diseases like metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atherosclerosis, neurodegenerative disease and pathogenic infection, particularly viral infection. The prostasin-like enzyme gene provides a therapeutic target of decreasing the enzyme activity, in particular for treating or preventing metastatic cancer. Neurodegenerative diseases in include for e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrapie. The agonists and antagonists of the polypeptide may be useful to treat osteoporosis, contagonists of the polypeptide may be useful to treat osteoporosis, antagonists of the polypeptide may be useful to treat osteoporosis, managonists of the polypeptide may be useful to treat osteoporosis, managonists of the polypeptide may be useful to treat osteoporosis, managonists of the polypeptide may be useful to treat osteoporosis, managonists of the progression of restenosis and atherosis. Anti-human prostasin-like enzyme activity inhibit the progression of restenosis and atherosis. Novel human prostasin-like enzyme polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and pathogenic biopsy specimens, plasma samples and body fluids. The present sequence represents a cDNA encoding a human prostasin-like serine protease like serine protease antibodies are useful for immunodetection and diagnosis of micrometastases, autoimmune lesions and renal failure in Sequence 944 BP; 150 A; 318 C; 318 G; 158 T; 0 U; 0 Other; Claim 1; Fig 5; 125pp; English. inflammatī infection.

243 213 124 CCGTACTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGGCTCAAACGCGCAGCCG 183 103 ecacacidecicereciaecas de arces de carces de cares de GAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGAC 363 ecacreccaecreaeraccecerececreesecrecerererererererexereredece 273 GGCGCGCACACCCGCGCAGTGGCCGCCATCGTGCCGGCCAACTACAGCCAAGTGGAG 423 274 cécacécricricegracicelráceacegeracrácrácicecegeacrácrices de 333 CTGGCCTGCGGGCAGCCCCGCATGTCCAGTCGGATCGTTGGGGGCCGGGATGGCCGGGAC 102 CTCATCGCCCCCTCCTGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTTG 303 GGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCC crearescecesaresarestas de consecuentes de consecuences de con 12; Query Match 20.5%; Score 226.4; DB 6; Length 944; Best Local Similarity 57.7%; Pred. No. 5.6e-31; Matches 448; Conservative 0; Mismatches 316; Indels 12 43 163 304 184 244

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ALIGNMENTS

AW450407 UI-H-BI3-akn-g-11-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone AW450407	AW450407.1 GI:6991183 BST.	Homo sapiens (human) Homo sapiens	Demonstration (Control of Charlets) (Sertebrats, Euteleostomi; Mammalis, Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 537)	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),	Tumor Gene Index	Unpublished (1997)	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Oligo-dT track not found, Not I site shown in beginning of sequence	is likely internal to the message. cDNA Library Preparation: M.B.	Soares Lab Clone distribution: NCI-CGAP clone distribution	information can be found through the I.M.A.G.E. Consortium/LLNL at:	www-bio.llnl.gov/bbrp/image/image.html	Seq primer: M13 Forward	POLYA=No.	Location/Qualifiers
RESULT 1 AW450407/C LOCUS DEFINITION ACCESSION	VERSION KEYWORDS	SOURCE		REFERENCE	AUTHORS	TITLE		JOURNAL	COMMENT									FEATURES
						redicted by chance to have a	core of the result being printed,	al score distribution.		IES			Description		AW450407 UI-H-BI3-	AI190509 qd49£07.x	AL551470 AL551470	BB850564 BB850564

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456 bp mRNA linear EST 28-OCT-1998

4849f07.x1 Soares fetal heart NDHH19W Homo sapiens cDNA clone
INAGE:1732837 3' similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLML; contact the
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (infr@mimage.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seg primer: -40UP from Gibco
High quality sequence stop: 452.
Location/Qualifiers
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/lab_host="DH10B (ampicillin resistant)"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1732837"
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llarity 99.6%; Pred. No. 6.5e-85;
Conservative 0; Mismatches 2;
                                                                       'organism="Homo sapiens"
'mol_type="mRNA"
'db xref="taxon:9606"
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AL551470 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI064YF02 5-PRIME, mRNA sequence.
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1 (bases 1 to 1071)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                         /clone="CSODIO64YF02"
/tissue type="PACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo (dT)
/note="lst prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7896.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI064DC010P1&cluster=7896.r. Contact
Feng Liang Email : filiang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI064DC01QP1.
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55.3%; Pred. No. 5.4e-28;
tive 1; Mismatches 374; Indels 16;
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                                                                                                                                                                                                                                                                                                                                          727 GACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTC 762
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/db_xref="taxon:9606"
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GGGCCCTTGTCCTGGGCCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGGCAGCTGGGGGCT

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433 bp mRNA linear EST 26-NOV-2001
BB850564 RIXEN full-length enriched, adult inner ear Mus musculus
EDNA clone F930108A18 5', mRNA sequence.
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Score 199.2; DB 10
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/clone="F930108E12"
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/strain="C57BL/6J"
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86.9%;
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Fax: 81-45-503-9216
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Carninol.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
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/clone_lib="RIKEN full-length enriched, adult inner ear"
                                 Hayarsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishli,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Maharyama,T., Nukamura,M., Nishli,K., Nomura,K., Numasaki,R., Okacaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Taqawa,A., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
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Anteniaki,Y.
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Flease visit our web site (http://genome.gsc.riken.go.jp) for
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/clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                           BB850607 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930108E12 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 433)
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381 AGTTCTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGAAGGAGGAGCGCACA 430
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayaka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kaukawa, T., Katoh, H., Kawai, J., Kojimi, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Mateuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazki, Y., Saito, R., Saitoh, H., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, T., Yoya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, T.
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ITGGGQWQSPGQWPWQVSITYDGWHVCGGSLVSNKWVVSAAHCFPREHSREXFYKLG
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ASFPIGLHCTWTGWGHVAPSYSLQTPRPLQQLEAVFISRETGSCLXNINAVPEEPPHI
QQDMLCAGYKGGQDAQCQDSGGSPLSCPREGIWYLAGIVSWGDACGAPNRFGVYTLTS
TYASWIHHHWAELQPRVVPGTQESQPDGHLCNHHPVFSSAAAPKLIRPVLFEFIGLTL
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product; PROSTASIN (SPTR|BABB2496,
evidence: FASTY, 98.5%ID, 100%length, match=1020)
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Please visit our web site for further details.
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|db_xref="MG1:2356949"
|db_xref="taxon:10090"
|clone="7530415E19"
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53.5%; Pred. No. 1.9e-24;
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/protein_id="BAC37362.1"
/db_xref="GI:26347427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length CDNAs
Nature 420, 563-573 (2002)
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                242 CCCTCATCGCCCCCTCCTGGGTCCTCTCGCTGCTCACTGTTCATGACGAATGGGACGT 301
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   0; Gaps
   Indels
      33;
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
      0; Mismatches
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HTC; CAP trapper.
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      219; Conservative
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SOURCE ORGANISM

AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

REFERENCE

JOURNAL MEDLINE PUBMED REFERENCE

TITLE

AUTHORS

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 6 AK078696

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//note="Organ: pooled colon, kidney, stomach; Vector:
//note="Organ: pooled colon, kidney, accorn destroyed; RNA pcWV-SPORT6; Site 1: Not1; Site, 2: EcoRV (destroyed), RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LiAMISG04 row: n column: 11
High quality sequence stop: 654.
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/clone="TMAGE:5759434"
/lab_host="DH10B"
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegani, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiwaji, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format gequencing pipeline with 384 multicapillary sequencer Sequence 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKO10640 1629 bp mRNA linear HTC 20-SEP-2003 Mus musculus Es cells cDNA, RIKEN full-length enriched library, clone:2410039E18 product:PROSTASIN, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 GGGCACCTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 TGGCACTTGGCCATGGCAGGTGAGCCTGCATCAAGGTGGGGGGCCACATCTGCGGGGGCTC
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Meth. Enzymol. 303, 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                                                                                                              Score 191.2; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
/organism="Mus musculus"
                                                                                                                         /db_xref="taxon:10090"
/clone="F930109F10"
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                                      /mol_type="mRNA"
/strain="C57BL/6J"
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Mus musculus (house mouse)
Mus musculus
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AK010640.1 GI:12846228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 AGGAGCGCACATGCGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                  17.48;
86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.7
Matches 222; Conservative
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Contact: Yoshihide Hayashizaki
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Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp,
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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1 (Bases It o 433)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Kojima, Y., Kouno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sagaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y., Watahiki, A., Yasunishi, A., RIKEN Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
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BB850795 RIXEN full-length enriched, adult inner ear Mus musculus cDNA clone F930109F10 5', mRNA sequence.
BB850795
        GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAG
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RESULT 8 BB850795 LOCUS

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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HPWGLHCTVYTGWGRYAPSVSLQTPRPLQQLEVPLISRETCSCLYNINAVPEEPHTIQ
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/db xref="G1:26370154"
/translation="WALRVGLGLGQLEAVTILLLLGLLQSGIRADGTEASCGAVIQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reseges.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                       Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNas
Nature 420, 563-573 (2002)
6 (bases 1 to 1629)
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                                                                                                                                                                                                                                          Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Hara, A., Hayareu, N., Hiramcto, K., Hiracka, T., Hori, F., Imotrani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Direct Submission
                                      RIKEN Genome Exploration Research Group Phase II Team and the
                                                                                                                                   the FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                        Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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/clone lib="RIKEN full-length enriched mouse cDNA
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/db_xref="MGI:1910128"
/db_xref="taxon:10090"
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/strain="C57BL/6J"
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DB 11; Length 1629;

16.3%; Score 180;

Query Match

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BI763558 861 bp mRNA linear EST 25-SEP-2001 603050292F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5190214 5', mRNA sequence..
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Pred. No. 7.4e-22;
0; Mismatches 415; Indels
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1. (bases I to 1010)
Statisty. Furumo, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawi, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, J., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, J., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, H., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D. P., Bult, C., Golobori, T., Schriml, L.M., Kanapin, A., Matsuda, H., Ratcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Tetcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Kawaii, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Marchionni, L., McKenzie, L., Mixil, I., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertca, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Red, D.J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sepule, C.A., Sectou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Vang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Wallains, L., Yuan, Z., Zavolan, M., Zhu, Y., Kawai, J., Aizawa, K., Azawa, T., Konno, H., Nakamura, M., Sato, K., Sato, K., Saraki, M., Marakawa, T., Makawa, T., Kagawa, T., Aizawa, K., Itoh, M., Kagawa, T., Miyazaki, A., Sakai, W., Intoh, M., Kagawa, I., Miyazaki, A., Sakai, W., Intoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.
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                                                           GAGCTGGGCCCGACCTGGCCGTGCGCGCGTGGCCTTCACCCGCCAGCCTGGGCCCCGCC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 767 TCTGGTACTGACGGGGCTTGTGAGCTGGGGACATGCCTGTGGGGGCCCGCACAGGCCTGGT 826
        347 GAGGACGCCAAGGTCAGCACCCTGAAGGACATCATCCCCCACCCCAGCTACCTCCAGGAG 406
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                     467 ATCCGGCCCATCTGCCTCCCTGCAACGCCTCCTTCCCCAACGGCCTCCACTGCACT
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                                                                                                         407 GGCTCCCAGGGGACATTGCACTCCTCCAACTCAGCAGACCCATCACCTTCTCCCGGTAC
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Mus musculus (house mouse)
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AUTHORS
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                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 861)
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                                                                                                                                                                                           1 (bases 1 to 861)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .861
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
BI763558
BI763558.1 GI:15755136
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                                                                                  Homo sapiens
                                                                                                         Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-1771 (2000)
Computer-based methods for the mouse full-length cDNA
computer-based methods for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="RIKEN full-length enriched, ES cells"
/clone lib="RikEN full-length enriched, ES cells"
/note="Site_1: XhoI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primed with a primer [5' GAGAGAGGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                              Laboratory for Genome Exploration Research Group, RIKEN Genomic Schences Center(GSC), Yokobama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                              Fax: 81-45-503-9216

Bmail: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp,

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,

Fukuda, S., Konno, H., Yoya, S., Miyazaki, A., Murata, M., Nakamura, M.

Nomura, K., Numazaki, R., Ohno, M., Obsato, N., Saito, R., Sakazume, N.,

Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y. Analysis of the mouse transcriptome based on functional annotation 6 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 16.7-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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1. 1010
/organism="Mus musculus"
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/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="2410035E18"
/cell type="RS cells"
/lab_host="SOLR"
                                                                                                                                                                                        Contact: Yoshihide Hayashizaki
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 429)
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97 GGGCCCTTGTCCTAGGCCATGGCCTTAAGGGTGGGCCTGGGACTTGGGCAGCTGGGACGCT
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KEYWORDS
SOURCE
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9

22;

0; Mismatches 387; Indels

469; Conservative Similarity

Local Best Loca Matches

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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
BP 191 9106 EVRY cedex - France
Invitrogen. This sequence belongs to sequence cluster 7995.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact :
Feng Liang Bmail : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001AD09FM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/organism="Homo sapiens"
/db xref=traxon;9606"
/clone="CSOCAP001YG17"
/clone="THYMUS"
/clone="Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotL-oligo(dr) primer. Five prime end enriched, with a NotLoligo(dr) primer. Five prime end enriched, with a Not I and ECORV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB593614 RIKEN full-length enriched, 4 days neonate male adipose Mus musculus cDNA clone B430104M11 5', mRNA sequence.
                                                                                                                                                       930 bp mRNA linear EST 15-MAY-2003
BX436299 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001XG17
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 930)
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EST.
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp/
Carninof.p., Shibata,Y., Hayatsu,M. and Hayashizaki,Y.
Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-22 Suebhiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 CCTAGACTGCGGCCGCCCCTGAGACCTCTTCCCGCATTGTGGGGGGGCTCGGACGCTCATCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 TGGAGCCCGCGGAATTGTCAGTTGTGCTGGGCGTGCACTCCCAGGACGGGCCCTGGA 417
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Haydseu,W.,M., Hiranoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Ishii,Y., Ito,M., Kawal,J., Kojima,Y., Komno,H., Kouda,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Matsuyama,T., Nakamura,M., Nishi,K., Sakai,R., Sakai,R.,
Sasaki,D., Sato,K., Shibata,K., Sakai,T., Sakai,T., Sakazume,N.,
Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RIKEN full-length enriched, adult inner ear"
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0; Mismatches 37; Indels
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/clone="F930101E02"
/tissue_type="inner ear"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
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Location/Qualifiers
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/strain="C57BL/6J"
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Best Local Similarity 84.4
Matches 205; Conservative
                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
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         80.2%;
     Best Local Similarity 80.2
Matches 199; Conservative
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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1 (bases I to 249)

2 Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Kodyama, Y., Imctani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Komno, H., Kusakae, M., Matsuyama, T., Miyazaki, R., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, R., Okazaki, Y., Shibata, K., Shibata, T., Shibata, Y., Shibata, T., Shibata, T., Shibata, T., Shibata, T., Yasunishi, F., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.

Intram Suzuki, M., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., RIKEN Mouse ESTS (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3/]. CDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site": Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adipose"
/dev_stage="4 days neonate"
/lab_host="DHIOB"
/clone_lib="RIKEN full-length enriched, 4 days neonate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:10090"
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musculus (house mouse)
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               ORGANISM
                                                                       REFERENCE
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GSS 15-JUN-2000
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Unpublished (1999)
Other GSSs: RPCI-23-466N15.TJ RPCI-23-466N15.TV RPCI-23-466N15.TVB
Contact: Shaying Zharyotic Genomics
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                              501 CCGCGCCTCACACCGCTTCGTGCACGCCACGCCTGCTGGGGCCACCGGCTGGGGAGACGT 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 CCAGGAGGCTGTCCCTCTGGCTCTGAGTTCTACAAGAAGTGGAGCTAAGGTTGGT 241
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Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de
Jong,P. and Fraser,C.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 430)
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
trp://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 466 row: N column: 15
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                                                                                                                                                                                           62 rchdchdcdcchddchdcchdchadchddadcchchchdrdcddddadchchdcchdcc
                                                            2 AGTGGCCACCATCCTGATACCGGAAACTACAGCACAGTGGAACTGGGCGCAGATTTGGC
                                                                                                                               381 AGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGGCGCCGACCTGGC
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RPCI-23-466N15.TJB RPCI-23 Mus musculus genomic clone RPCI-23-466N15, genomic survey sequence.
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/strain="C57BL/6J"
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/clone="RPCI-23-466N15"
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selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                   40 AGGGTGACTCTGGGGGACGCCTGGTCTGTGAGGACGGAGGCCGATGGTTCCTGGCCGGAA 99
                                                                                                                                                            737 AGGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCGCTGGTTCCAGGCAA
                                                                                                                                                                                                                                  797 rcaccagcririgegririgecrgragaacgagaaaacgcccrggagririgacrgrag
                                                                                   Query Match 15.3%; Score 168.6; DB 28; Length 430;
Best Local Similarity 88.4%; Pred. No. 5.1e-20;
Matches 183; Conservative 0; Mismatches 24; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                             917 CCACCCAGCCCCAGAAGACCCCAGTCAG 943
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Search completed: February 25, 2004, 11:17:42 Job time : 2791 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
         Copyright
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February 25, 2004, 08:23:39; Search time 112 Seconds (without alignments) 5460.320 Million cell updates/sec Run on:

sw model

using

nucleic search,

OM nucleic

US-10-037-417-45

1102 Perfect score:

Title:

1 gggcccttgtcctgggccat......gggggttctgatggggcctcc 1102 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 seqs, 277475446 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

1365418

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:* Issued_Patents_NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	100	Sequence 8, Appli Sequence 8, Appli		H	30,	431	'n	256	256		15, 7	25	w,	œ	59	H	H	Sequence 18, Appl	ń	18	15	70	22	17.	Sequence 18, Appl	13,
SOMMAKIES	US-09-387-375-1	-09-38/-3/5-	9-386-642-	-09-386-	09-023-	09-620-	US-09-023-942A-5	39-907-794A-2	US-09-905-125A-256	US-09-902-775A-256	US-09-008-271A-15	US-09-023-942A-25	US-09-023-942A-3	US-09-386-653A-8	US-09-386-642-59	US-09-027-337-1	US-09-644-600-1	US-09-644-600-18	US-09-654-600A-1	US-09-654-600A-18	US-09-023-655-157	US-09-280-116-107	US-09-016-366A-22	US-08-978-404B-17	US-09-016-366A-18	US-08-978-404B-13
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Sequence 20, Appl Sequence 15, Appl Sequence 1, Appl Sequence 11, Appl Sequence 11, Appl Sequence 262, App Sequence 262, App Sequence 262, App Sequence 9, Appl Sequence 9, Appl Sequence 28, Appl Sequence 10, Appl Sequence 11, Appl Sequence 20, Ap
US-09-016-366A-20 US-08-978-404B-15 US-09-079-970A-4 US-09-079-970A-1 US-09-970A-16 US-09-970A-16 US-09-970A-16 US-09-905-125A-262 US-09-905-125A-262 US-09-905-125A-262 US-09-905-125A-262 US-09-905-125A-262 US-09-027-386-629-2 US-09-654-600A-9 US-09-664-600A-9 US-09-186-629-2 US-09-186-629-2 US-09-286-116-10 US-09-280-116-10 US-09-280-116-10
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ALIGNMENTS

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129 CTGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGGCAGCCGGGCAC 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.3%; Score 224; DB 4; Length 1613; Best Local Similarity 57.9%; Pred. No. 1.1e-41; Matches 442; Conservative 0; Mismatches 310; Indels 1;
                                                                                            GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Gi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Proctease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT FILING DAIE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
                                                  Sequence 1, Application US/09387375
Patent No. 6485957
                                                                                                                                                                                                                                                                                                                                                          PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 1
US-09-387-375-1
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248

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Farent No. 6420157;
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Farent No. 6420167;
Farent Normannon:
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT FILING DATE: 1999-08-31;
NUMBER OF SEQ 1D NOS: 60
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APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jonson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
TITLE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT APPLICATION NUMBER: US/09/387,375
CURRENT AILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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19.7%; Score 216.8; DB 4;
Best Local Similarity 58.0%; Pred. No. 4.1e-40;
Matches 427; Conservative 0; Mismatches 297;
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LENGTH: 1130
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APPLICANT: Darrow, Andrew; APPLICANT: Darrow, Andrew; APPLICANT: Qi, Jian-shen; TITLE OF INVENTION: DNA encoding the novel human serine; TITLE OF INVENTION: protease T; FILE REFERENCE: ORT-1032; CURRENT APPLICATION: UNMERR: US/09/386,653A; CURRENT FILING DATE: 1999-08-31; NUMBER: Patentin Ver. 2.0; SOFTWARE: Patentin Ver. 2.0; SET DATE: 1110
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No. 1.8e-28;
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APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
APPLICANT: Andrade-Gordon, Parricia
TITLE OF INVENTION: Zymogen Activation System
FILE REPRENCE: ONE-1028
FULE REPRENCE: ONE-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1169
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Sequence 30, Application US/09023942A

Patent No. 6479274

GENERAL INFORMATION:

APPLICANT: (US only) ANTALIS Toni Mari

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
         Conservative
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CITY: GARDEN CITY
STATE: NEW YORK
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APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION NUMBER: P0422/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P0422/97
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,346
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Pred. No. 2.9e-28;
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......: US/09/023,942A
13-FEB-1998
.w. 435
                      Patentin Release #1.0,
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 436
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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54.2%;
SOFTWARE: Patentin Relea CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFILIAG DATE: 13-FEB-1998 CLASSIFICATION: 435
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Best Local Similarity
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289 ACGAATGGGACGTTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAG 348
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APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF INSENUES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
FILING DATE: 13-FEB-1998
CLASSIFFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PO5101/97
FILING DATE: 13-FEB-1997
FILING DATE: 13-FEB-1997
FILING DATE: 18-FEB-1997
FILING DATE: 18-FEB-1997
FILING DATE: 18-NOV-1997
FILING DATE: 18-NOV-1997
FILING DATE: 18-NOV-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09023942A Patent No. 6479274
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530 TGGCTACCAACCATCAAGAATGACATGCTGTGGGCCGCTTCGAGGAGGCAA 589
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                                                                                                                                        CAGGGACACCTGCCAGGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCGCTG
                                                                                                                                                                                                                           590 GAAGGATGCCTGCAAGGGCGACTCGGGCGCCCCCTGGTGTGTGCTCCTGGGTTCTGTG
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14.7%; Score 162; DB 4; Length 1212;
Best Local Similarity 53.6%; Pred. No. 9.4e-28;
Matches 414; Conservative 0; Mismatches 340; Indels 1
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TITLE OF INVEXTION: No. 65696621 Nucleic Acids and
TITLE OF INVEXTION: No. 65696621 Nucleic Acids and
TITLE OF INVEXTION: No. 65696621 Nucleic Acids and
FILE REFERENCE: 784CTP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: US/0552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE PL-LEGENES VETSION 1.0
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Patent No. 6569662
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
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Wehrman, Tom
Xue, Aidong J.
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; LOCATION: (135)..(1007)
US-09-620-312D-431
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ORGANISM: Homo sapiens
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US-09-620-312D-431
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
ATTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                     824 GICIACACCAAIAICAGCCACCACIIIIGAGIGGAICCAGAAGCIGAIG
                                         841 GITITCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTG
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CURRENT APPLICATION NUMBER: US/09/907,734A
CURRENT RILING DATE: 2001-07-17
PRIOR PELLOR DATE: 2000-02-22
PRIOR PELLORATION NUMBER: US 60/143,048
PRIOR PELLORATION NUMBER: US 60/145,698
PRIOR PELLORATION NUMBER: US 60/146,222
PRIOR PELLORATION NUMBER: US 60/146,222
PRIOR PELLORATION NUMBER: PCT/US99/2054
PRIOR PELLORATION NUMBER: PCT/US99/2059
PRIOR PELLORATION NUMBER: PCT/US99/2059
PRIOR PELLORATION NUMBER: PCT/US99/2059
PRIOR PELLING DATE: 1999-09-08
PRIOR PELLING DATE: 1999-09-15
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RRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 256, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Filvaroff, Ellen
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Roy, Margaret Ann
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Gerritsen, Mary E.
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Mather, Jennie P.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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International PCT Application
                                                                                                                                                                                                 REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
TELEFAX: (516) 742 434
TELEFAX: 230 901 SANS UR
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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52.9%;
                                               FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGLIO, FRANK S
REGISTRATION NUMBER: 31,
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Best Local Similarity 52.9<sup>5</sup>
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Pred. No. 1.1e-27;
0; Mismatches 344; Indels 18;
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILLING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Gaps
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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Pred. No. 1.1e-27;
0; Mismatches 344;
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-03
                                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth, J.
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Best Local Similarity 52.9%;
Matches 406; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                              Pan, James
Paoni, Nicholas F.
Ferrara, Napoleone
Filvaroff, Ellen
                                                                                                                                                     Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                        Kljavin, Ivar J.
Mather, Jennie P.
                                                                                                                         Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart, Truncament, Daniel
                                                                                               Wei-Qiang
                                                                  Sherman
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ORGANISM: Homo Sapien
                                                                                                                                                                                        Goddard, A.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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Sequence 256, Application US/09905125A Patent No. 6664376 GENERAL INFORMATION:

US-09-905-125A-256

APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi

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Transmembrane Polypeptides and Nucleic
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Secreted and Transmembrane
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/02,775A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-01-15
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-07
                                                                                                                                                           Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                            Pan, James
Paoni, Nicholas F.
                                    Kljavin, Ivar J.
Mather, Jennie P.
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APPLICANT:
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APPLICANT:
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TGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGCACC 189
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                                                           296 cccrcccccrcccrccarccrcarccraccraccrarccarccarccrarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarccarc
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130 TGCGGGCGCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGCACC 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 GCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTTGGAGCCC 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 TGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGGCTCCCTCATC
                                                                                                                                                                                                                                                            Length 1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                   Score 161.6; DB 4;
Pred. No. 1.1e-27;
0; Mismatches 344;
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llarity 52.9%;
Conservative
; ORGANISM: Homo Sapien
US-09-902-775A-256
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 406; Conserv
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Sequence 256, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:

RESULT 11 US-09-902-775A-256 Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L.

APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi APPLICANT: Botstein, Davi Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L.

APPLICANT

Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A.

APPLICANT: APPLICANT:

Ferrara, Napoleone Filvaroff, Ellen

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

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52.7%; Pred. No. 2.6e-27;
ive 0; Mismatches 345; Indels
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                                                      REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458
TELECOMMUNICATION INFORMATION:
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US-09-008-271A-15
                Mohan-Peterson, Sheela
                                                                                                                                                                                                   TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUTO3
CLONE: 789927
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Matches 405; Conservative
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296 CCCTCCGGGTGGATGGTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/008,2718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown>
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Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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US-09-008-271A-15
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APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CARESPONDENCE ADDRESS: ADDRESSER. SCULLY, SCOTT, MURPHY & PRESSER
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,942A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 13-FEB-1998
CLASSIFICATION: 435
IOR APPLIANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 11168
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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   Sequence 25, Application US/09023942A
Patent No. 6479274
GENERAL INFORMATION:
APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David TITLE OF INVENTION:
NOVEL MOLECULES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: ADDRESSER
STREET: NOW GARDEN CITY PLAZA
CITY: GRANDEN CITY
STATE: NEW YORK
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SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
US/09/023,942A
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FREERENCEATION NUMBER:
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ilarity 52.4%; Pred. No. 8.8e-27;
Conservative 0; Mismatches 334;
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELERAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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nucleic acid
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Matches 377; Conserv
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US-09-023-942A-25
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9-023-942A-25
                                                                                                                                                                                                                                                                                                           CITY: GAB
STATE: NE
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
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199 CTGGACAGTCCAGTTTGGTGAGCTGACTTCCAGGCCATCTCTGGAACCTACAGGCCTA 258
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                                                                                                            369 GCACACCCGCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGG 428
                                                                                                                                                                                                                                                                                                                                                                                                                     319 CAATGACATAGCCCTGCTGAAGCTGTCATCTCCCAGTCACCTACAATAACTTCATCCAGCC
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                                                                                                                                                                                                                                                                                                                    COCCGACCTGGCCCTGCTGCCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGGCC
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GCGCACACCCCCCCCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTG 426
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                                                                                                                                                                                                                                                                                                                                                                                                              14.0%; Score 154.8; DB 4; 52.2%; Pred. No. 3.9e-26; ive 0; Mismatches 352;
TELEFAX: (516) 742 4343
TELEFAX: (516) 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1094 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 52.2
Matches 398; Conservative
                                                                                                                                                                                                                                                                                                                                    17..955
                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 17.
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14.0%; Score 153.8; DB 4; Length 1
Best Local Similarity 53.9%; Pred. No. 6.6e-26;
Matches 392; Conservative 0; Mismatches 317; Indels
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TITLE OF INVENTION: DA encoding the novel human serine
TITLE OF INVENTION: DA encoding the novel human serine
TITLE OF INVENTION: protease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NOS
LENGTH: 1130
; Sequence 8, Application US/09386653A ; Patent No. 6458564
                                                                                       APPLICANT: Andrade-Gordon, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                        Darrow, Andrew
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Search completed: February 25, 2004, 11:19:47 Job time : 118 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Sequence 52, Appl	Sequence 447, App		Sequence 25, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2214, Ap	Sequence 141, App	Sequence 261, App	Sequence 208, App	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli
£	1D	US-09-888-615-52	US-10-101-510-447	US-10-176-847-85	US-10-051-874-25	US-10-041-400A-1	US-10-041-264A-1	US-10-042-091A-1	US-09-948-094-1	US-09-880-107-2214	US-09-967-768A-141	US-10-097-340-261	US-09-925-301-208	US-10-041-400A-8	US-10-041-264A-8	US-10-042-091A-8
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                                                                             APPLICANT: PLOWARM, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CHANFDELL, SEAN
APPLICANT: CHANFDCZAK, GLEN
APPLICANT: CHANFDCZAK, GLEN
APPLICANT: CHANFDCZAK, GLEN
APPLICANT: WIDARSANM, SUCHA
APPLICANT: WIDARSANM, SUCHA
TILLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 52
SEQ ID NO 52
               ; Sequence 52, Application US/0988615; Patent No. US20020064856A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-888-615-52
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US-10-176-847-85

Sequence 85, Application US/10176847

Publication No. US20030068636A1

GENERAL INFORMATION:

APPLICANT: Veiby, Petter Ole

TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
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Pred. No. 2.4e-51;
0; Mismatches 401; Indels
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Fublication No. US2030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF 17
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2002-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATCHT NOS: 805
SEC ID NO 447
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Best Local Similarity 55.0
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APPLICANT: SCORE, DATE OF
TITLE OF INVENTION: CATHERINE E
TITLE OF INVENTION: URING THE SAME
FILE REPERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/269,595
PRIOR APPLICATION NUMBER: 60/269,597
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR PELING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/262,454
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/276,777
PRIOR APPLICATION NUMBER: 60/230,336
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-01-18
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906 GTGTACACTCTGGCCTCCAGGTATGCCTGGATCCAAAGCAAGGTGACAGAACTCCAG 965
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APPLICATION UNMBER: 60/330,336
ELING DATE: 2001-10-18
APPLICATION NUMBER: 60/265,530
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APPLICATION NUMBER: 60/261,376
                                                                                                                        CCTGGGCCTGCCTTTCCCCACCCAG
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APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
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Herrman, John L
Peyman, John A
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Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
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Taupier Jr, Raymond
Gerlach, Valerie
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Edinger, Shlomit R
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Tchernev, Velizar
Zerhusen, Bryan D
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Liu, Xiaohong
Ellerman, Karen
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Smithson, Glennda
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Shenoy, Suresh G
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Stone, David J
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Pred. No. 5.9e-51;
0; Mismatches 402;
        TITLE OF INVENTION: AND OVARIAN CANCER FILE REFREENCE: MRI-039 CURRENT APPLICATION NUMBER: US/10/176,847 CURRENT FILING DATE: 2002-06-21 NUMBER OF SEQ ID NOS: 112 SOFFWARE: PASLSEQ for Windows Version 4.0 SEQ ID NO 85 LENGTH: 1733
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Best Local Similarity 54.9

Matches 507; Conservative
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PRIOR FILING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
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Sequence 1, Application US/10041400A Publication No. US20020110895A1 GENERAL INFORMATION:
APPLICANT: Darrow, Andrew APPLICANT: Andrade-Gordon, Patricia

RESULT 5 US-10-041-400A-1

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FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
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Pred. No. 3.6e-49;
0; Mismatches 310; Indels 12
                                               Sequence 1, Application US/10041264A

Publication No. US20020142446A1

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
CURRENT APPLICATION NUMBER: US/10/041,264A

CURRENT APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
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Conservative (
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; Publication No. US20020142447A1
; Publication No. US20020142447A1
; GENERAL INFORMATION:
    APPLICANT: Darrow, Andrew
; APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
; TITLE OF INVENTION: DNA Encoding the Human Serine
; TITLE OF INVENTION: Protease EOS
; FILE REFERENCE: ORT-1031
; CURRENT APPLICATION NUMBER: US/10/042,091A
; CURRENT PAPLICATION NUMBER: US/09/387,375
; PRIOR PILING DATE: 2002-01-08
; PRIOR FILING DATE: 1999-08-31
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APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE PATENTION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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US-09-880-107-2214
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54.2%; Pred. No. 2e-48;
sive 0; Mismatches 408;
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Best Local Similarity 54.2%;
Matches 501; Conservative
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APPLICANT: Horne, Darci T.
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LENGTH: 1834
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| Patent No. US20020090625A1
| GENERAL INFORMATION:
| APPLICANT: The Brigham and Women's Hospital, Inc.
| APPLICANT: Wong, Kwong-kwok
| APPLICANT: Wong, Kwong-kwok
| TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
| FILE REFERENCE: 81994/282423
| CURRENT APPLICATION NUMBER: US/09/948,094
| NUMBER OF SEQ ID NOS: 4
| SOFTWARE: Patentin Version 3.0
| SEQ ID NO 1
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US-09-948-094-1
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PC1/US00/05882
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
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LIENGTH: 1668
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TITLE OF INVENTION: Massessment, Prevention, and Therapy of Ovarian Cancer
FILE REPREMENTE: MRI. 030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT PILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR PLICATION NUMBER: 60/256,149
PRIOR PLICATION NUMBER: 60/256
PRIOR FILING DATE: 2001-03-14
PRIOR PLICATION NUMBER: 60/326
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PLICATION NUMBER: 60/311,732
PRIOR PLICATION NUMBER: 60/311,732
PRIOR PLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PESTSEQ for Windows Version 4.0
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Pred. No. 2e-48;
0; Mismatches 408; Indels
                                                               1096 CCTCGTGTGCCCCCAAACCCAG 1119
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, Sequence 261, Application US/10097340

; Publication No. US20030087250A1

; GENERAL INFORMATION:
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APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Stubhangi KANATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Machael MORRISEY
APPLICANT: Peter OLANDT
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54.2%;
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Robert C. BAST, Jr.
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Xumei ZHAO
Karen GLATT
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Best Local Similarity 54.2
Matches 501; Conservative
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ENGTH: 1834
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OTHER INFORMATION: Description of Artificial Sequence: Nucleic acid

CTHER INFORMATION: sequence of EOS zymogen fusion gene
US-10-041-400A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT APPLICATION NUMBER: US/09/387,375
PRIOR APPLICATION NUMBER: US/09/387,375
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                  1076 GCCTCGTGTGCCCCAAACCCAA 1100
                            924
                                  GCCTGGCCTGCCTTTCCCACCCAG
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10041400A, Publication No. US20020110895A1 (GENERAL INFORMATION: APPLICANT: Darrow, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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427; Conservative
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Pred. No. 2.8e-48;
2; Mismatches 401;
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CTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature 1.0CATION: (1598)
CTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature 1.0CATION: (1620)
CTHER INFORMATION: n equals a,t,g, or US-09-925-3101-208
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Best Local Similarity 54.7%;
Matches 506; Conservative
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                                                                         577 creccagagegegacederacadadeadraageracederecrecregadreecedaderee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
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Publication No. US20020142446A1

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: QI, Jenson
TITLE OF INVENTION: Drotease EOS
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: UNMBER: US/10/041,264A
CURRENT APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
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Matches 427; Conservative
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Search completed: February 25, 2004, 12:28:25 Job time : 457 secs

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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U., Rothenberg,M., Stone,D., Shonoy,S. and Anderson,D. Proteins and nucleic acids encoding same
Patent: WO 02053742-A. 45 11-JUL-2002;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Rothenberg, M., Stone, D., Boldog, F., Shenoy, S. and .
Proteins and nucleic acids encoding same
Patent: WO 02053742-A, 43 11-JUL-2002;
Curagen Corporation (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1102; Conservative 0; Mismatches
                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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      GAGCTGGGCGCCGACCTGGCCCTGCTGCGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCC
                                                                                                             GAGCTGGGCCCCGACCTGGCCCTGCTGCCTCACCCGCCAGCCTGGGCCCCGCC
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Plowman, G., Whyte, D., Sudarsanam, S.,
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Sugen, Inc. (US)
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Sequence 52 from Patent WO0200860.
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1. 2457
/organism="Homo sapiens"
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AUTHORS
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                                                                 CIGCCITTCCCACCCAGCCCCAGAAGACCCAGICAGAI
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .2810
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TETSUJI OTSUKI, HISASHI KOGA
                                                                                                                                                                                                                                                                    Primer for synthesizing
BD127529
                                                                                                                                                                                                                                                                                                                BD127529.1 GI:23222474
JP 2002017375-A/2960.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHINICHI KOJIMA
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrbini; Hominidae; Homo.
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                                                                                    Yue, H., Azimzai, Y., Kallick, D.A., Baughn, M.R., Griffin, J.A., Swarnakar, A., Lal, P.G., Walia, N.K., Hafalia, A.J., Gandhi, A.R., Au-Young, J., Blloct, V.S., Ramkumar, J., Thangavelu, K., Lu, Y., Warren, B.A., Lu, D.A., Lee, E.A., Tribouley, C.M., Arvizu, C., Delegeane, A.M., Yao, M.G., Khan, F.A. and Sanjanwala, M.M. Protein modification and maintenance molecules

Patent: WO 0245383-A 31 13-JUN-2002;
Incyte Genonics, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Incyte ID No: 2751509CB1"
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                            Incyte Genomics, Inc. (US)
   Location/Qualifiers
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Best Local Similarity 99.8%;
Matches 816; Conservative
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                                                                    REFERENCE
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JP 2002017375-A/2960
22-JAN-2002
07-UJL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAXASHI, SHIZUKO
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C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
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CIGCIGIGGCTACCTATGAGGCATGGATACGGGAGCAGGGGGATGGGTTCAGAGCCTGGGC 889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. (bas. 1 to 2010)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 IGGCCACATCTGCGGGGGCTCCTCATCGCCCCTCCTGGGTCCTCTCCGCTGCTCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 GGGGGGCTCAAACGCGCAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koga,H.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2960 22-JAN-2002;
HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                         2810 bp DNA linear PAT 1 full-length cDNA and use thereof.
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AVPLPGDPPHALCPAYOEKEEVGSCWNDSRWSLLCQBEGTWFLAGIRDFPSGCLRPRA
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                                                                                                                                          /tissue type="placenta"
/clone Tib="PLACE1"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                      300. .2600
/note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAC11431.1"
/db_xref="GI:22761041"
organism="Homo sapiens"
                                                                                                        lone="PLACE1005003"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKO75142 2810 bp mRNA linear PRI 03-SEP-2002 Homo sapiens CDNA FLJ90661 fis, clone PLACE1005003, weakly similar to PROSTASIN PRECURSOR (EC 3.4.21.-).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens (human)
Homo sapiens
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NEDO human cDNA sequencing project
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Isogai, T. and Otsuki, T.
Direct Submission
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Primer for synthesizing full-length cDNA linear PAT 18-SEP-2002 BD125219 BD125219 GI:23220164 DEFE BD125219.1 GI:23220164 DEFE BD1202017375-A/650.
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
117 CTTCAACCTCACTCTCCAGATAITGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGCCG 58
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Regulation of human prostasin-like serine protease
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                  DNA
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/mol_type="unassigned DNA"
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                                                                                                                                                                                                                          Sequence 3 from Patent W00198467.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 GIGGCCTGTCTGCCCCGCGCCCCCACACGCTTCGTGCACGGCACCGCCTGCTGGGGGC
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                                                                                                                                   CCTCATCGCCCCCCCCTCCTGGGTCCTCTCCGCTGCTCACTGTTTCATGACGAATGGGACGTT
     CTGTGAGGAAGGGGCCGCTGGTTCCAGGCAGGAATCACCAGCTTTGGCTTTTGGCTTTTGGCTGTGG
                                                                                   822 ACGGAGAAACCGCCCTGGAGTTTTCACTGTGGGCTACCTATGAGGCATGGATACGGGA
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Regulation of human prostasin-like serine protease Patent: WO 0198467-A 1 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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99.8%; Pred. No. 7.3e-245;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX342934 537 bp Sequence 1 from Patent WO0198467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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Best Local Similarity 99.8
Matches 536; Conservative
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ACCESSION
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SOURCE
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558 205 618 145 678

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Euteleostomi;

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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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127769 bp DNA linear PRI 29-MAR-2003
Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
AC009088.9 GI:29366934
                                                                                                                                                                                                                                                                                                                                                                                                                 C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length CDNA and use thereof FH Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 ITICALGAAGGAAGGITGGAGCCCGCGGGGCCGAGTGGTCGGTACTGCTGGCGTGCA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           356 CICCCAGGACGGCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCC 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            402 GGCCAACTACAGCCAAGTGGAGCTGGGCGCCGACCTGGCCCTGCCGCCTGGCCTCACC 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GGCCAACTACAGCCAAGTGGAGCTGGGGCCGACCTGGCCCTGCTGCGCCTGGCGCCTACACCCA75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCCCAGGACGGGCCCCTGGACGGCGCACACCCGGCGCAGTGGCCGCCATCGTGGTGCC 401
                                                                                                                                                                                                                             22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                             C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 670)
Ota.T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 TGGCCACATCTGCGGGGGCTCCCTCATCGCCCCCTCCTGGGTCCTCCGCTGCTCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCCAGCCTGGGCCCGTGTGGCCTGTCTGCCTGCCCCGCGCGCCTCACACCGCTTCGT
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                                                                                                                                                                                                                                                                                                  YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI,
                                                                                                                           Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 1916 22-JAN-2002;
HELIX RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism='Homo sapiens (human)'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 670;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31.4%; Score 346; DB 6; I
99.7%; Pred. No. 6.3e-171;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .670
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                            TETSUJI OTSUKI, HISASHI KOGA
                                                                                                                                                                                         Homo sapiens (human)
JP 2002017375-A/1916
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                                                                                                                                                                                                                                                                                                          PI YURI KAWAL,
SHINICHI KOJIMA,
    Homo sapiens
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                                                                                                                  Koga, H.
                                                                                                                                                                                           PP
PP
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ACCESSION
VERSION
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AC009088/c
  ORGANISM
                                                                                                                                   TITLE
JOURNAL
                                                      REFERENCE
AUTHORS
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                                                                                            Parimer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 650 22-JAN-2002;
Patent: MESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/650
PP 22-JAN-2002
PP 07-JUL-2000 JP 200253172
PT TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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                                                                                                                                                                                                                                                                                                                  PI TETSUJI OTSUKI,HISASHI KOGA
PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
                                                                                                                                                                                                                                                                                                                                                                                   C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCCACATCTGCGGGGGCTCCTCATCGCCCCCTCCTGGGTCCTCCCCTGCTGCTG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401
                                                                                                                                                                                                                                                                        PI
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 670)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 TGGCCACATCTGCGGGGGCTCCCTCATCGCCCCCTCTGGGTCCTCTCCGCTGCTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCAGCCTGGGCCCCCCCCCGCGTGTGTCTGCCTGCCCCGCGCCTCACACGCTTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 GGGGGGCTCAAACGCGCAGCCGGGCACCTGGCCAAGTGAGCCTGCACCATGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                            PI ISHII,
PI YURI KAWAL,AI WAKAMATSU,TOMOYASU SUGIYAMA,KBIICHI NAGAI,
SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BD126485
Primer for synthesizing full-length cDNA and use thereof. BD126485
BD126485.
GI:23221430
JP 2002017375-A/1916.
Homo sapiens (human)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 346; DB 6; Length 670;
Pred. No. 6.3e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Submitted (05-OCT-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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1 (bases 1 to 195476)

105 Joint Genome Institute.

Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consensus quality: 171229 bases at least Q40
Consensus quality: 182638 bases at least Q30
Consensus quality: 188055 bases at least Q30
Consensus quality: 188055 bases at least Q20
Estimated insert size: 170000; agarcose-fp estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agarcose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                 AC135044 195476 bp DNA linear HTG 05-C
HOWO saptens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
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Center clone name: CITB-E1_2551B20
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Center Code: JGI
Web site: http://www.jgi.doe.gov
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Finishing Completed at Stanford Human Genome Center and Los Alamos
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National Laboratory
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Wuw-shgo.stanford.edu
Bstimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 233.4kb). It is clipped at the overlap with AC135050.
The number of bases overlapped is 2575.
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Submitted (03-APR-2002) Production Sequencing Facility, DOB Joint
Genome Institute, 2900 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 127769)
DOB Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
Direct Submission
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Chases 1 to 127769)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

Submitted (129-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Mar 29, 2003 this sequence version replaced gi:29029216.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 127769)

DOB Joint Genome Institute, Stanford Human Genome Center and Los
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100.0%; Pred. No. -...
0; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="t=xon:9606"
/chromosome="16"
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DOE Joint Genome Institute.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                             Drive, Walnut Creek, CA 94599, USA
Drive, Walnut Creek, CA 94599, USA
On Mar 19, 2003 this sequence version replaced gi:21702833.

Draft Sequence Produced by DoE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Location/Qualifiers
                                                           3 (Dases 1 to 168064)
Dob Joint Genome Institute.
Direct Submission
Submitted (197-JUN-2002) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases 1 to 168064)
Direct Submission
Submitted (07-JUL-2002) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Openome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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94598, USA
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DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
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Direct Submission
Submitted (31-AUG-2001) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
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100.0%; Pred. No. 2.5e-34;
ive 0; Mismatches 0;
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Millennium Predictive Medicine, Inc.
Location/Qualifiers
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AX098193.1 GI:13515276
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Organism="Homo sapiens"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
Direct Submission
Unpublished
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DOB Joint Genome Institute.
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Homo sapiens chromosome 16 clone RP11-120K18, complete sequence.
AC093520
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                      39003: contig of 6084 bp in length 39103: gap of unknown length 48470: contig of 9267 bp in length 48470: gap of unknown length 5922: contig of 11251 bp in length 5922: gap of unknown length 72404: gap of unknown length 72404: gap of unknown length 85449: contig of 12483 bp in length 101872: contig of 12945 bp in length 101872: contig of 12483 bp in length 101972: gap of unknown length 11776: gap of unknown length 11776: gap of unknown length 118973: contig of 12104 bp in length 119973: gap of unknown length 1193073: contig of 12104 bp in length 150336: contig of 121037 bp in length 150336: contig of 12103 bp in length 150336: contig of 45040 bp in length 150336: contig of 45040 bp in length 150336: contig of 45040 bp in length
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// Organism="Homo sapiens"
// mol_type="qenomic DNA"
/db_xref="taxon:9606"
/chromosome="lch"
/clone="CID-2551B20"
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         length
bp in length
length
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larity 100.0%; Pred. No. 5.6e-131;
Conservative 0; Mismatches 0;
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Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
                                                                                                                                                                                                                                                   BC001462 1800 bp mRNA linear PRI 04-OCT-2003 Homo sapiens protease, serine, 8 (prostasin), mRNA (cDNA clone MGC:2133 IMAGE:3138532), complete cds.
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Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                     GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTTCCTGGGGGCCTGGGGCAGCTGGGGGCT
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (INSC),
Galthersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
on Aug 19, 2003 this sequence version replaced gi:12655206.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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     Length 1796;
                                    0; Indels
                   1.3e-23;
      DB 6;
6.1%; Score ... 1.36
100.0%; Pred. No. 1.36
ive 0; Mismatches
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                   similarity 100.
                                                                                                                                                                   194 GTGGCCA 200
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                                                                                                                                    GIGGCCA 67
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     Query Match
Best Local 8
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                    RESULT 15
BC001462
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                                    Matches
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KEYWORDS
SOURCE
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COMMENT
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SFPNGLHCTVTGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPERPHFVQ
EDMYCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASS
                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIAN at: http://image.llnl.gov Series: IRAL Plate: 4 Row: j Column: 3 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YASWIQSKVTELQPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG
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McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Placenta, choriocarcinoma"
/clone_llb="NH WGC 21"
/lab_host="DH10B-R"
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100.0%; Pred. No. 1.3e-23;
live 0; Mismatches 0;
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176. .1207
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GenCore version 5.1.6
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February 25, 2004, 11:17:50; Search time 475 Seconds (without alignments) 9855.820 Million cell updates/sec Run on:

US-10-037-417-45 1102 Title:

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Gapop_60.0 , Gapext 60.0 OLIGO NUC Scoring table:

3373863 segs, 2124099041 residues Searched:

Total number of hits satisfying chosen parameters: 0 Word size :

6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

N Geneseq 29Jan04:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004s:*

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SUMMARIES

	Description	4	Abq93902 Human pro	Abk31795 DNA encod	Human	Aak94500 Human ful	Abk13565 Human pro	Aas69040 DNA encod	Abk13566 Human pro	Aak92190 Human cDN		Aah78206 Nucleotid	Aas71079 DNA encod	Abt31936 Human bre	8 Human	Aaf98720 Human lat	Human	Abn85392 Human NOV	Abs76501 cDNA enco	σ	o.		CDNA	Abn95716 Gene #221
SOMETHING	A	ABQ93901	ABQ93902	ABK31795	ABQ75956	AAK94500	ABK13565	AAS69040	ABK13566	AAK92190	AAK93456	AAH78206	AAS71079	ABT31936	AAF98698	AAF98720	ABZ35336	ABN85392	ABS76501	ABL67949	ABL68512	ABL68248	ABK12241	ABN95716
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ė	Çuery Match	100.0	100.0	65.0	65.0	57.3	44.1	36.1	34.8	31.4	31.4	12.3	12.3	6.1	6.1	6.1	6.1	4.8	4.8	4.8	4.8	4.8	4.8	4.8
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Aai29377 Colon tum Abz33563 Human col Aba21236 Human ner Abn85393 Human NOV	Human Human Human Human	Abx73450 Human nov Abk13570 Prostasin Abq93931 Human NOV Abs52114 Human bet	Drosop Drosop Drosop Human	ADK-01224 Human KLK ADQ83347 Human KLK ADA95896 Human KLK ADK31801 DNA encod ADK30259 Human G-p ADK30258 Human G-p
AAI29377 ABZ33563 ABA21236 ABN85393	AAC77814 AAC26531 ABX73872 AACS6109	ABX73450 ABK13570 ABQ93931 ABS52114	ABL29631 ABL29630 ABL18082 AAD27724	ABK30252 ABQ83347 AAA95896 ABK31801 ABK30259 ABK30258
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ALIGNMENTS

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Human; NOVX; neurological disorder; Alzheimer's disease;

Huntington's disease; Parkinson's disease;

Huntington's disease; Parkinson's disease;

Addiction; tuberous sclerosis; cancer; immune disorder;

allergy;

Autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

Andomeriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;

pancratitis; cirrhosis; glomerular endotheliosis; bacterial infection;

polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

Antherosclerosis; call signal processing—related disorder;

metabolic pathway regulation disorder; oytostatic; neuroprotective;

antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic;

dermatcological; antibacterial; antiarthritic; hepatotropic; neurogenesis;

differentiation; proliferation; motility; heamatopoiesis; wound healing;

anglogenesis; forensic biology; transgenic animal; drug screening;

metaboy; NOV14a; prostatin precursor-like; chromosome 16; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                    Human prostatin precursor-like NOV14a DNA, SEQ ID NO:43.
                                                                                                 BP.
                                                                                                 ABQ93901 standard; DNA; 1102
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                             01-NOV-2002
                                                                                                                                                                                                       ABQ93901;
RESULT 1
                                                   ABQ93901
                                                                                                                                                    RANGE STATE STATE
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Location/Qualifiers ๗ 19. .1050 1. .18 /*tag= /*tag= Homo sapiens. Key 5'UTR CDS

/partial /product= "NOV14a" /note= "No stop codon given in the specification"

WO200253742-A2

11-JUL-2002.

05-JAN-2001; 2001US-0260018P. 08-JAN-2001; 2001US-0260360P. 28-FEB-2001; 2001US-0272411P.

07-JAN-2002; 2002WO-US000375

CCCCCGTACTGCGGGCGCCCTGAGCCCTCGGCCCCGCATCGTGGGGGGCTCAAACGCGCAG 180

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02-MAR-2001; 2
05-JUL-2001; 2
12-JUL-2001; 2
                                                      Query Match
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ij á Kekuda R, Alsobrook JP, Tchernev VT, Liu X, Spytek KA; Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U; Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson Padigaru M, Taupier RJ, Miller CE, Bisen A; 05-JTJ-2001; 2001US-0303231P. 12-JTJ-2001; 2001US-0305660P. 10-SEP-2001; 2001US-0318405P. 12-SEP-2001; 2001US-0318700P. 04-JAN-2002; 2002US-0037417. (CURA-) CURAGEN CORP.

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WPI; 2002-583619/62. P-PSDB; ABB09523.

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

Claim 9a; Page 142; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14

(ABB09501-ABB09524), collectively referred to as NOVX proteins, and
mucleic acids encoding them (ABQ03879-ABQ03902). NOVX proteins and
mucleic acids encoding them (ABQ03879-ABQ03902). NOVX proteins and
conditions are useful in the treatment, diagnosis or prevention of NOVXassociated disorders or in the manufacture of a medicament for treating
cuch disorders, based on their homology to known proteins. Various
disorders are associated with NOVX proteins including neurological
disorders are associated with NOVX proteins including neurological
disorders are additional disorders, addition, tuberous sclerosis, cancers
cc disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases),
cc disorders and autoimmune disorders encorations and parkinson's abune.
cc de-g., Appertension), reproductive disorders, endometriosis,
cc de-g., Appertension), reproductive disorders, endometriosis,
cc de-g., Appertension), reproductive disorders, endometriosis,
cc de-g., Appertension), reproductive disorders, and particularly cardiomyopathy,
cc disorders, obesity, bacterial infections and particularly cardiomyopathy,
disorders, obesity, bacterial infections and particularly cardiomyopathy,
cd alsorders, obesity, bacterial infections and particularly cardiomyopathy,
disorders, obesity, bacterial infections and particularly cardiomyopathy,
cd therosclerosis, cell ular receptors or downstream effectors which
continuing to a NOVX protein, and are also useful as targets for the
contribution, haemacopoiesis, wound healing and angiogenesis. NOVX
contribution and cloning NOVX homolegues in other cell or threateners and condens are useful for studying the function and
creates and a source of primers or probes for forensic biology and creativity of NOVX proteins and for identifying and cloning NOVX homolegues in other cell price are useful for studying the function and created or chromosome 16
cc prostatin precursor-like protein NOVI4a. The gene encoding NOVI4a is

Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other;

DB 6; Length 1102;

ö 9 9 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCCT ececernerecrissecentesecensaassesserecrissesererseseeneseer 0; Gaps 0; Indels 100.0%; Score 1102; 100.0%; Pred. No. 0; iive 0; Mismatches Best Local Similarity 100. Matches 1102; Conservative à g

GIGGCCAATICTGACTCATATTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGC 120

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780 780 840 840 900 540 540 900 009 099 099 720 720 360 420 420 480 480 GTTTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATCAGAG CCTGGGCCTGCCTTTCCCCACCCCAGAAGACCCCAGTCAGATTGTTTACATCAAACG ccidedecteccinicalectedeceaaaaaccaataantinininaaaacaaaaaaaaaaa GCATTCCTGGATTCTGCCAGAATCCTTTTGAGGCCCTTGTCCCATATATCAGTAGGAGTC 721 cecheceacacereceacereacrerececececerererereaceacece TGGTTCCAGGCAGGAATCACCAGCTTTGGGTTTGGCTGTGGACGGAGAAACCGCCCTGGA GITITICACTGCTGTGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAG 961 GCAITCCTGGATTCTGCCAGAATCCTTTTGAGGCCCTTGTCCCATATATCAGTAGGAGTC TCAACTGGGACCAAAAGCCTTGTCCTCCCCTGGCTCTCTCCACACTCTCTCCTGGGCCTTC cogecaccroscrategrandrandrandcaccracardenderccacararrardendes CGCAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCGC recerearesecrecarecarecrereces accreaterrange and recent and a second a second and a second a second and a second a second and a second a second and a second a second and a second a second and a second a sec recercandececerecresererereserserererererererexes TIGGAGCCCGCCGAGTGGTCGGTAACTGCTGGGCGTGCACCCCCAGGACGGCCCCTG GACGGCGCGCACACCCGCCAGCGCCCCATCGTGGTGCCGGCCAACTACAGCCAAGTG GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTCCCCTCCCCTGGGTGCTACAG gecacedecressasadacerecassassasaderasarecerereceressassassas CCCTTCAACCTCACTCCCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGC 661 CCCTICAACTCACTCACCAGATATTGCCAGGGATGCTGTGTGCTGGCTACCAGAGGGGC TIGGAGCCCGCGGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTG da de masacacaca a respecta de masacaca de contra cocaca de contra GIGIGGCCIGICTGCCTCCCGCGCCTCACCGCTTCGTGCACGGCACCGCCTGCTGG CCGGGCCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC TGGGGGTTCTGATGGGGCCTCC 1102 781 841 1021 1081 901 901 196 541 481 541 601 601 661 721 301 361 421 481 241 301 121 181 181 à g 셤 à g g à Dp ₽ 원 à 셤 à d ò ď ò ਨੋ a ò 셤 δ g à 엄 à d ð a ð ₽

ABQ93902 standard; DNA; 1102 RESULT 2
ABQ93902
ID ABQ93

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(first entry)

Huntington's disease; Parkinson's disease; pain; behavioural disorder; addiction; tuberous sclerosis; cancer; immune disorder; allergy; autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

Human; NOVX; neurological disorder; Alzheimer's disease; Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45.

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX-associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 thyroiditis, cardiovascular disease, hypertension; reproductive disorder; endometriosis; incontinence; psoriasis; seleroderma, alopecia; ulcer; endometriosis; incontinence; psoriasis; seleroderma, alopecia; ulcer; pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection; polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy; atherosclerosis; cell signal processing-related disorder; operoprotective; metabolic pathway regulation disorder; cyrostatic; neuroprotective; antiinflammatory; immunosuppressive; analgesic; antiatherosclerotic; dermatological; antibacterial; antiarthritic; hepatotropic; neurogenesis; differentiation; proliferation; motility; hematopolesis; wound healing; angiogenesis; forensic biology; transgenic animal; drug screening; gene therapy; NOV14b; prostatin precursor-like; gene; de. Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune CAM, Grosse WM, Lepley DM, Burgess CE, Ve. Inger S, Sciore P, Ellerman K, Malyank, Stone D, Boldog F, Guo X, Shenoy S, Taupier RJ, Miller CE, Eisen A; Claim 9a; Page 143; 323pp; English. Location/Qualifiers /product= "NOV14b" 1093. .1102 /*tag= c 08-JAN-2001, 2001US-0260360P.
28-FEB-2001, 2001US-0272411P.
05-UAR-2001, 2001US-0272817P.
05-UUL-2001, 2001US-0303231P.
12-UUL-2001, 2001US-030560P.
10-SEP-2001, 2001US-031840SP.
12-SEP-2001, 2001US-031840SP.
04-JAN-2002, 2002US-0037417. 07-JAN-2002; 2002WO-US000375 /*tag= a 19. .1092 /*tag= b Kekuda R, Alsobrook JP, l. .18 /*tag≈ Patturajan M, Grosse Gorman L, Edinger S, Rothenberg M, Stone D (CURA-) CURAGEN CORP 2002-583619/62. P-PSDB; ABB09524 WO200253742-A2 Homo sapiens 05-JAN-2001; Padigaru M, disorders Key 5'UTR 3'UTR

CC disorders are associated with NoVX proteins including neurological disorders are associated with NoVX proteins including neurological cdisorders (e.g., Alzheimer's, Huntington's and Parkhison's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., allergies and autoimmune diseases), wastchenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, asthma, continence, psoriasis, scleroderma, alopecia, ulcers, pancreatis, circontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatis, circontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatis, circontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatis, cell signal processing-related disorders endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NoVX mucleic acids and polypeptides may be used to identify cellular receptors or downstream effectors which binds to a NoVX protein, and are also useful as targets for the identification of small molecules that modulate or inhibit processes such is not ifferation, haematopoiesis, wound healing and angiogenesis. NoVX cucleic acids sequences can be used to identify a cell or tissue type and are useful as a source of primers or probes for forensic biology and for identifying and cloning NoVX homologues in other cell types. Cells comprising NOVX mucleic acids are useful for studying the function and current sequence represents DNA encoding the present sequence represents DNA encoding the present sequence represents DNA encoding the prostatin precursor-like protein NOV14b 888888888888888888888888888888888

Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other;

GIGIGGCCIGICTGCCCGCGCGCCCTCACCGCTTCGTGCACGGCACCGCCTGCTGG 540 360 GAGCTGGGCGCCGACCTGGCCGCCTGCGCCTCACCCGCCAGCCTGGGCCCCGCC 480 009 trasascecesces de respectos de la constanta de la secono de la constanta del constanta de la constanta del constanta de la constanta del constanta del constanta de la constanta del constanta del constanta del constanta del constanta del c 420 480 120 120 180 180 240 300 recerchteececereregereeredecreerekererreargadaardeake 300 9 GACGGCGCGCACCCGCCAGTGGCCGCCATCGTGCCGGCCAACTACAGCCAAGTG GCCACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGGTGCTACAG GACGGCGCACACCCCCCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTG 1 gescerrierereseceareseceasaasesesereresesecresecaseaseres 61 GTGGCCAATTCTGACTCATACTCACTTTACGGGTTGGTGCCGTCCGGACCCGCTAGGGGC 61 GIGGCCAAIICIGACTCAIACICACIIIAAGGGTIGGIGCCGICCGGACCCGGIAGGGGC CCCCCGTACTGCGGGCGCCTTGGGCCCTCGGCCTGGGGGGGCTCAAACGCGCAG TCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCTTCTTCATGACGAATGGGACG TTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCCAGGACGGGCCCCTG CCGGGCCACCTGGCCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGC 1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGCCT Gaps ò 6; Length 1102; Indels ö DB 100.0%; Score 1102; 100.0%; Pred. No. 0; 0; Mismatches Best Local Similarity 100. Matches 1102; Conservative 121 241 361 361 421 481 481 181 181 241 301 301 421 Query Match 쉱 ð 엄 à ð d g à 셤 ð g ð à à

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Nucleic acids encoding novel human proteases, useful for useful

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and disorders (e.g. inflammatory thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, pain, sexual dysfunction, mood disorders (e.g. rennion disorders, pain, sexual dysfunction, mood disorders, attention disorders, hypotension, hypertension, psychotic disorders, neurological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (b.g. virus (HIV), and mon-viral infections caused by human immunodeficiency colors and and mon-viral infections such as ocular disease (e.g. virus (HIV) and mon-viral infections can be accounted to the color of the colors of
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treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory disorders.
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Claim 5; Page 196; 200pp; English

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Lal PG, Walia NK, Hafalia AJA, Gandhi AR, Au-Young J, Elliott VS;
Ramkumar J, Thangavelu K, Lu Y, Warren BA, Lu DAM, Lee EA;
Tribouley CM, Arvizu C, Delegeane AM, Yao MG, Khan FA;
Sanjanwala MM;
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21-DBC-2000; 2000US-0257803P.
05-JAN-2001; 2001US-026010P.
19-JAN-2001; 2001US-0264623P.
25-JAN-2001; 2001US-0264623P.
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New isolated Protein Modification and Maintenance polypeptides, useful for diagnosis, and treatment of e.g. gastrointestinal disorders.

WPI; 2002-519664/55. P-PSDB; ABB98135.

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The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptide. Polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. en) typertension), autoimmune/inflammatory disorders (e.g. anaemia), cell hypertension), neurological disorders (e.g. Alzheimer's disease) creproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the creffects of exagenous compound on the expression of nucleic acid and amino acid sequence represents a human PMMMM encoding sequence of the invention, encoding a polypeptide which has been found to have homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the prince of the production, but was obtained in CD-ROM format directly
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                            CTGCCTTTCCCACCCAGCCCCAGAAGACCCCAGTCAGAT
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss.
                                                           895
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                                                                                                                             ACGGAGAAACCGCCCTGGAGTTTTCACTGCTGTGGCTACCTATGAGGCATGGATACGGGA
                                         Human prostasin-like serine protease cDNA #1.
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Matches

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Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.

Claim 1; Fig 1; 111pp; English.

This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypahn-like serine protease is useful fluid. An antibody specific for prostasin-like serine protease; autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of used to modulate enzyme activity in a disease, such as metastasis of used to modulate enzyme activity in a disease, such as metastasis of cust to protein amyloid plaques of Genstmann-Straussler Syndrome, creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral creating protein amyloid plaques of Genstmann-Straussler Syndrome, creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral creapeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The activity, in particular for treating or preventing metastatic cancer. The augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants cortivity dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnases for detecting diseases and abnormalities or susceptibility to assays for detecting diseases and abnormalities or susceptibility to assays for detecting diseases and abnormalities or susceptibility to prostasin-like serine protease #1 nucleotide sequence of the invention

Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other;

ö 482 362 418 422 302 478 358 ceneareseceretrassreererecerecereserererereareacearesecer GGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGA 477 dehiciciocidecidadidencedinarieneses de describios de decribios de describios de decribios de describios de de CGGCGCGCACACCCGCGCCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGA 417 CGGCGCGCACACCCGCGCAGTGGCCGCCATGGTGGTGCCGGCCAACTACAGCGAAGTGGGA GCTGGGCCCGACCTGGCCCCTGCCGCCTGGCCTCACCCGCCAGCCTGGGCCCCGT CCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGCTCACGTTCATGACGAATGGGACGTT Gaps . Length 537; 1; Indels 44.1%; Score 486; DB 6; I 99.8%; Pred. No. 1.1e-216; iive 0; Mismatches 1; Local Similarity 99.8 les 536; Conservative 243 537 303 363 423 Query Match Matches

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers. Oilgomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding pattners are useful in medical imaging of sites expressing (II). (I) are useful for treating disorders involving aberrant protein expression or biological activity. The CTICAACCICACICICCAGGATATIGCCAGGGATGCTGTGTGCTGGCTACCCAGAGGGCCG 722 602 662 cricaacticacticicadarafreccadedargirerererecreecracedadedede CAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCG 779 357 GCIGGGCCCGACCIGCCCTGCCCTGCCTCACCCGCCAGCCTGGGCCCCGCT GIGGCCIGICIGCCCCCCCCCCCCCCCCCCTCCGIGCACGCCACCCCCTGCTGGGC CACCGGCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGA CAGGGACACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGGGGCCC 1 Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess DNA encoding novel human diagnostic protein #4844. Claim 1; SEQ ID NO 4844; 103pp; English. ВР Tang YT; 30-MAR-2001; 2001WO-US008631. 31-MAR-2000; 2000US-00540217 23-AUG-2000; 2000US-00649167 AAS69040 standard; cDNA; 597 (first entry) Liu C, WPI; 2001-639362/73 (HYSE-) HYSEQ INC P-PSDB; ABG04853. WO200175067-A2 biodiversity. Drmanac RT, Homo sapiens 13-FEB-2002 11-OCT-2001. AAS69040; 297 237 603 177 663 543 117 723 57 483 RESULT 7 AAS69040 g g 쉱 ₽ à à g ò à

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23-JUN-2000; 2000US-0213588P 20-MAR-2001; 2001US-0276909P

WPI; 2002-114576/15.

Morozov V;

Xiao Y,

(FARB) BAYER AG

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polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity
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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; censtmann. Straussler Syndrome; viral infection; Scrapie; Creutzfeldt. Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss; EST; expressed sequence tag.
                                                                                                                              Human prostasin-like serine protease cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001WO-EP007117.
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                   08-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                 27-DEC-2001
                                                                  ABK13566;
RESULT 8
ABK13566/c
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GGTGACTCTGGGGGGCCCCTGGTC 762

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This invention comprises the cDMA and protein sequences of an isolated prostasin-like serine procease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypshin-like serine protease is useful fluid. An antibody specific for prostasin-like serine protease; autoimmune lesions and renal failure in diagnosis of micro-metastases, autoimmune lesions and renal failure in biopsy speciments, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (CODB), atherosclerosis, neurodegenerative disease (CoPB), atherosclerosis, neurodegenerative disease activity, in particular for treating or infection, particularly viral infection. The human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The augment and inhibit the henzyme activity which may be useful to treat corteoporosis, Paget's disease and degradation of bone implants of particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibit the progression of restenosis and and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic diseases related to the presence of mutations in mucleic acid sequences which encode the enzyme. The present sequence represents the human control protease #2 nucleotide sequence of the invention
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                                                                                                                                                                                                                                                                                     Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGGCGAGGCCACCTGTCAATGTCTCTACAGCCAGCCCGGTCCCTTCAACCTCACTCTC
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Pred. No. 4.7e-16
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 384; Conservative
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The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the CDNA. The full length clones were obtained by construction of full length enriched CDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA assily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a CDNA construction. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO TITCATCACCAATCCCACCTIGGAGCCCGGGGCCGAGTGGTCGGTTGCTGGGGGGGTGCA 341 CICCORGGACGGGCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCATCGTGGTGCC 401 830 Primers useful for synthesizing full length cDNA clones and their use TGGCCACATCTGCGGGGGGCTCCTCATCGCCCCCTCGGGTCCTCTCGCTCACTG TGGCCACATCTGCGGGGGCTCCCTCATCGCCCCCTCTGGGGTCCTCTCCGCTGCTCACTG 162 gggggggttgaaacgcgggagcggggaccrggccrrrggcaagrgaggcaccarggagg Ota I, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga Claim 2; SEQ ID NO 650; 1380pp + Sequence Listing; English. Human; full length cDNA; cDNA synthesis; oligo-capping; ss. Sequence 670 BP; 97 A; 245 C; 205 G; 118 T; 0 U; 5 Other; 1; Indels 31.4%; Score 346; DB 4; I 99.7%; Pred. No. 2.6e-151; tive 0; Mismatches 1; SEQ ID NO: 650. 11-JAN-2000; 2000JP-00118774. 02-MAY-2000; 2000JP-00183765. 99JP-00194486 AAK92190 standard; cDNA; 670 07-JUL-2000; 2000EP-00114089 Human cDNA 5' -end sequence, 396; Conservative (first entry) genetic manipulation. (HELI-) HELIX RES INST. WPI; 2001-524255/58 Query Match Best Local Similarity 08-JUL-1999; Homo sapiens EP1130094-A2 06-NOV-2001 05-SEP-2001 222 236 282 296 342 AAK92190; Matches 'n RESULT 9 AAK92190 엄 à д ò d ð

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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                                                                                             521
                                                                                                                            535
356 CICCCAGGACGGCCCCTGGACGGCGCGCACACCCGCGCAGTGGCCGCCAICGTGGTGCC 415
                                                                                             462 GGCCAGCCTGGGCCCCGCCGTGTGGCCTGCCTGCCCGCGCCTCACACCGCTTCGT
                                                                                                                  GGCCAACTACAGCCAAGTGGAGCTGGCCGGACCTGGCCCTGCTGCCTGGCCTCACC
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                   Human cDNA clone representative sequence, SEQ ID NO: 1916.
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K, Kojima S, Otsuki
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                                                                                                                                                                                          536 dchcddchcdcchdchddchdddchddddag 572
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a T, Nagai
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2000JP-00118774.
2000JP-00183765.
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11-JAN-2000;
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162 GGGGGGCTCAPACGCGGCGCGCGCCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGG 221

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Length 670;

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                                                                                            GGCCAACTACAGCCAAGTGGAGCTGGGCGCCGACCTGGCCCTGCGCCTGGCCTCACC 461
                                                                                                                                                                                                        475
                                                                                                                             401
176 GGGGGCTCAAACGCGCAGCCGGGCACCTGGCCAAGTGAGCCTGCACCATGGAGG 235
                         TGGCCACATCTGCGGGGGGTCCCTCATCGCCCCTCCTGGGTCCTCTCCGCTGCTCACTG 281
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                                                                            282 TTTCATGACGAATGGGACGTTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a human secreted polypeptide.
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/product= "secreted polypeptide"
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2000US-0236874P.
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P-PSDB; AAG67514.
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03-OCT-2000;
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The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polynucleotides are useful for treating nervous and consultations and metastasis, for muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating classases in spinal cord, thyroid gland, ovary, prostate, renal gland, candle intestine, heart, trachea, thyrwus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and colon, for treating lipase deficiency in cystic fibrosis and constitution for treating undesirable clot formation such as myocardial confarction, during angioplasty and all surgical procedures that require confarcased blood clot formation, for treating limmume disorders, for treating inflammation and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 ATCGTGGGGGCTCAAACGCGCCAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCAT 216
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     Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immut disorders, microbial diseases, inflammation and transplant rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #6883.
                                                                              Claim 2; Page 44-45; 102pp; English
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 100.
Matches 135; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of (II) or to treat disease states involving expressed control of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal control for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food (II) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The colypeptide and polynucleotide sequences have applications in caping identification of mutations of against types of data and products dependent on DNA and amino acid sequences. Aa&&4197-AA&$94$64 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this coding sequences of the invention. Note: The sequence data for this content the printed specification, but was obtained in the content of the conte
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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100.0%; Pred. No. 8.6e-53;
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                                                                                                                   Claim 1; SEQ ID NO 6883; 103pp; English
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Matches 135; Conservative
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21-JUN-2001; 2001US-0300159P. 27-JUN-2001; 2001US-0301351P.

(MILL-) MILLENNIUM PHARM INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (I) (see AAF98594 to AAF98730), in a patient sample; and (2) the normal level of expression of (I) in a control non-ovarian cancer sample,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGCCCTTGTCCTGGGCCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                Determining the presence of breast cancer in an individual, involves using specific polynucleotide markers.
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100.0%; Pred. No. ...
... 0; Mismatches
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                                                                                                                                                                                                            Disclosure; Page 192-193; 233pp; English
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21-MAR-2000;
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20-JUL-2000;
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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see AAF98594 to AAF98730), in a patient sample, and (2) the mornal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (I) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer
where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. (I) have cytostatic activities and can be used in antisense gene therapy. The method, compositions and kits from the present invention can be used for: (I) assessing and treating ovarian cancer; (2) making isolated hybridoma, which produces an antibody useful for ovarian cancer assessment; and (3) inhibiting ovarian cancer in a patient. AAF988573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                       1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAACTGGGGGCT
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tumour; kinase; marker; cytostatic; antisense gene therapy; ds.
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                                                                                                                                                                                          Sequence 1796 BP; 327 A; 599 C; 511 G; 359 T; 0 U; 0 Other;
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o. 5e-21;
o. indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human late stage ovarian tumour polynucleotide marker 28.
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                                                                                                                                                                                                                                                     1 Similarity 100.0%; Pred. No. 5e-67; Conservative 0; Mismatches
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                                                                                                                                                                                                                                   Score 67;
Pred. No.
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16-MRR-2000; 2000US-0190347P.
21-MRR-2000; 2000US-0191321P.
31-MRY-2000; 2000US-020382P.
20-JUL-2000; 2000US-00220467.
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assessment; and (3) inhibiting ovarian cancer in a patient. AAF98573 to AAF98593 represent human kinase marker primers and probes which are used in the exemplification of the present invention
                                                                                                                                  Gaps
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                                                                                                     Length 1835;
                                                                 Sequence 1835 BP; 309 A; 621 C; 527 G; 378 T; 0 U; 0 Other;
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                                                                                                   Score 67; DB 5;
Pred. No. 5e-21;
                                                                                                               100.0%; Pred. No.
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AI190509 qd49f07.x
BX436299 BX436299
AA300017 EST12620
                                                              February 25, 2004, 12:18:11; Search time 2783 Seconds (without alignments) 11824.694 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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9 AI190509
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                                            OM nucleic - nucleic search, using sw model
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ALIGNMENTS

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/geve="unknown"
/geve stage="19 weeks"
/dev stage="19 weeks"
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/clone_organ.
/clone
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456 bp mRNA linear EST 28-OCT-1998

qd49f07.xl Soares fetal heart NbHH19W Homo sapiens cDNA clone
IMAGE:1732837 3' Similar to SW:NCP6_MOUSE P21845 MAST CELL PROTEASE
6 PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 456)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
106 CTCTCCAGATATTGCCAGGATGCTGTGTGTGCTGGCTACCCAGAGGCCGCAGAGACACCCT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 452.
Location/Qualifiers
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34.8%; Score 384; DB 9; Length 456;
Best Local Similarity 100.0%; Pred. No. 1.6e-170;
Matches 384; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                     46 GCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAAGGCGGCC 1
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AI190509.1 GI:3741718
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Unpublished (1997)
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/lab host="UMAGE:273503"
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/clone=lih="UNCI CGAP Sub5"
/note="Vector: pi773D-Pac Fire line NCI CGAP Sub5
is a subtracted library derived from NCI CGAP Sub5
is a subtracted DNA preparation of NCI CGAP Sub4. The
NCI CGAP Sub5 library had 3 million recombinants. A
NCI CGAP Sub5 library had 3 million recombinants. A
NCI CGAP Sub5 library derived from NCI CGAP Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE Pool (NCI CGAP Kid3 Pool 1 LLAM
3334-3337, 3662-3663, 3798-3803 (IMAGE CloneIDS
1322376-1323911, 1456008-1456775, 1500552-1502855);
NCI CGAP Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778
(IMAGE CloneIDS 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI CGAP Lu5 pool 1 LLAM 3575-3582,
3881-3854 (IMAGE CloneIDS
164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDS
1127928-1240615); NCI CGAP Lu5 pool 1 LLAM 257-2459, 2758-2759, 3062-3068
(IMAGE CloneIDS 985608-986759,1101192-1101959,
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE CloneIDS 985608-986759,1101192-1101959,
NCI CGAP Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE CloneIDS 986508-986759,1101192-1101959,
NCI CGAP Sub1 (IMAGE CloneIDS 2710536-2712455) and
NCI CGAP Sub1 (IMAGE CloneIDS 2710536-2712455)
NCI CGAP Sub4 (IMAGE CloneIDS 2712456-2712455)
(10% of the driver population), plus a pool of 1,736-2712455)
NCI CGAP Sub4 (IMAGE CloneIDS 2712456-2712455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GAGACGICCAGGAGGCAGAICCICIGCCICCCCCCGGGIGCIACAGGAAGIGGAGCIAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CICICCAGAIATIGCCAGGGAIGCIGIGGIGGCIACCCAGAGGGCCGCAGGGACACCI 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          466 CCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGACGCGCGCACAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           494 GCCTGCCCGCGCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGGGCCACCGGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 434 ACCIRGCCCIGCCIGCCCIGGCCICACCCGCCAGCCIGGGCCCCGCCGIGIGGCCIGICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                346 ACCTGGCCCTGCTGCCTGCCTCACCGCCAGCCTGGGCCCCGCCGTGTGGCCTGTT
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al Similarity 100.0%; Pred. No. 2.5e-209;
466; Conservative 0; Mismatches 0;
                                                             1. .537
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG TISSUE=colon
TAG LIB=NCI CGAP CO10
TAG SEQ=AAACG"
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      674
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Homo.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae. Homo.

RS Adams, M.D., Karlavage, A.R., Fleischmann, R.D., Fuldner, R.A., J.D., Bult, C.J., Elee, J.A., Blace, J.A., Brandon, R.C., Man-Wai, C., White, O., Sutton, G., Blace, J.A., Brandon, R.C., Man-Wai, C., Fitzgerald, L.M., Fitzgerald, L.M., Fitzchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hannah, M.C., Hedblom, E., Hinkle, P. S.Jr., Glodek, A., Gnehm, C.L., Hannah, M.C., Hedblom, E., Hinkle, P. S.Jr., Moreno-Palanques, R.F., McDonald, L.A., Ngyuen, D.T., Pelligrino, S.M., Moreno-Palanques, R.F., McDonald, L.A., Ngyuen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bhillips, C.A., Ryder, S.E., Caoba, Cepeda, M.A., Coleman, J.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Rozak, D.L., Kunsch, C., Hungjun, J., Hit, Meissner, P. S., Olsen, H., Raymond, L., Wei, Y. Wing, J.C., Yu, G.L., Raben, S.M., Dillion, P.J., Farnon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Inital assessment of human gene diversity and expression patterns based upon 83 million nucleocides of cDNA sequence

M. Nature 377 (6547 Suppl), 3-174 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 3018699423
Fax: 3018699423
Fax: 3018699423
Fax: Solution availability, additional sequence and expression
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse
Location/Qualifiers
                                                                                                                            EST 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/note="Organ: uterus; Vector: pBluescript SK-; Site_1:
BookI; Site_2: Xhol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGGCTTGGGGGCT
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                                                                                                                              AA300017 294 bp mRNA linear EST 18-2
EST12620 Uterus tumor I Homo sapiens CDNA 5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
The Institute for Genomic Research
The Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Best Local Similarity 100.0%; Pred. No. 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Other ESTS: EST12621 THC176739
Contact: Kerlavage, AR
                                                                                                                                                                                      prostasin, mRNA sequence.
                                                                                                                                                                                                                 AA300017.1 GI:1952347
EST.
226 AAGACCCAGTCAGAT 240
                                                                                                                                                                                                                                                                              Homo sapiens (human)
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PUBMED
COMMENT
                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                   DEFINITION
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                                                                                                 RESULT 4
AA300017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 igganacgagadcagangangagantcagaccrasscratecrarecaccascccas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 TITGGCIGTGGACGAGAAACCGCCCTGGAGTTTTCACTGCTGTGGCTACCTATGAGGCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                   930 bp mRNA linear EST 15-MAY-2003
BX436299 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP001YG17
3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bulkaryore, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bulkaryore, Metheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 930)

1 (bases 1 to 930)

1 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

1 Full-length cDNA libraries and normalization

Contact: Genoscope
                                                                                                                                                                                              679 CAGATATTGCCAGGATGCTGTGTGTGCTGGCTACCCAGAGGGCCGCAGGGACACCTGCCAG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact
Feng biang Email: fliang@lifetech.com WEL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001AD09FM1.
Location/Qualifiers
                                                                                                        678
                                                                                                                                             144 crasscandectacciarchararerectacceaececsarectrenaecteaece
                                                                                                                                                                                                                        Genoscope - Centra National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Inbrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                 GTCCAGGAGGCAGATCCTCTCTCTCCCCTGGGTGCTACAGGAAGTGGAGCTAAGGCTG
                                         204 GICCAGGAGGCAGAICCICTGCCICTCCCCTGGGIGCIACAGGAAGTGGAGCIAAGAGCG
                                                                                                        CTGGGCGAGGCCACCTGTCAATGTCTCTACAGCCAGCCCGGTCCCTTCAACCTCACTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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llarity 100.0%; Pred. No. 1.4e-52;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    739 GGTGACTCTGGGGGGCCCCTGGTC 762
                                                                                                                                                                                                                                                                                                                                 24 GGTGACTCTGGGGGGCCCCTGGTC 1
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Homo sapiens
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Matches 135; C
                               559
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ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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BX436299
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

DEFINITION

RESULT 5 BM828821

ACCESSION

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Query Match
6.1%; Score 67; DB 9; Lk
Best Local Similarity. 100.0%; Fred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0;
                                                                                          AI393077
AI393077.1 GI:4222624
                                                                                                                                          Homo sapiens (human)
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A1623099
LOCUS
DEFINITION
                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                      LOCUS
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TITLE
                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                               REFERENCE
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AI393077
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/ cell_type="Spithelial"

/ cell_type="Spithelial"

/ cell_type="Spithelial"

/ cell_type="Toplof"

/ lab host="Toplof"

/ clone lib="SSSNU601"

/ clone lib="SSSNU601"

/ clone lib="SSSNU601"

/ lote 2: Xho!; The poly (A)+ RNA was dephosphorylated with Site 2: Xho!; The poly (A)+ RNA was dephosphorylated with tabacco acid pyrophosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with Sfil and cloned into DraIII- digested pMEISS-FIJ vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
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                                                                                                BM828821 318 bp mRNA linear EST 06-MAR-2002
K-EST0101694 S9SNUG01 Homo sapiens CDNA clone S9SNUG01-51-E07 5',
                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 1.9e-20;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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                                                                                                                                                                                  BM828821.1 GI:19185230
                                                                                                                                                                                                                       Homo sapiens (human)
Homo sapiens
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Best Local Similarity 100.
Matches 67; Conservative
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                                                                                                                                                MRNA sequence.
                218 GTGGCCA 224
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9

RESULT :

g ð

ORIGIN

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
Tissue Procurement: Ash Alizadeh, John Byrd, M.D.,
M.D., Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Masshington University Genome Sequencing Center
DNA Sequencing by: Masshington University Genome distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/lange/image.html
Innert Length: 691 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 334.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T 31; double-grranded CDNA was ligated to Eco RI addaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
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tg5sf08.xi NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109831 3'
similar to SW:PSS8_HUMAN Q16651 PROSTASIN PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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1 (bases 1 to 360)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Thumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGCCTGGGCAGCTGGGGGCT
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A1623099.1 GI:4648024
EST.
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 406)
Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 bp mRNA linear EST 28-JAN-2003
K-EST0161920 L7N800102 Homo sapiens CDNA clone L7N800102-4-C01 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTTCCTGGGGCCTGGGCAGCTGGGGGGT
      Contact: Sobert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 763 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 6.1%; Score 67; DB 9; Length 377;
1 Similarity 100.0%; Pred. No. 1.9e-20;
67; Conservative 0; Mismatches 0; Indels
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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Fax: +82-42-860-4409
Email: yongenngmail.kribb.re.kr
Plate: 4 row: C column: 01
High quality sequence stop: 406.
High quality sequence
                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                      Insert Length: 763 Std Error:
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Location/Qualifiers
1. 377
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CB116948.1 GI:27942755
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Genome Research Center
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Unpublished (1997)
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Best Local Similarity
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JOURNAL
COMMENT
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   JOURNAL
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                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.

Emmert-back, M.D., Ph.D.

EDNA Library Preparation: M. Bento Soares, Ph.D.

EDNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbr/finage/finage.html

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/note="Organ: pr22 was prepared, and ss normalized library NOT CGAP_Pr22 was prepared, and ss circles were made in viro.—Following HAP_purification, this DNA was used as tracer in a subtractive hybridization traction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 98508-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (Sase 1 to 377)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 366)
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                                                                                                                                               NCT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .366
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/dev_stāgē="adult"
/clome_lib="male adult skin, full-length enriched
chimpanzee cDNA library"
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6.1%; Score 67; DB
Best Local Similarity 100.0%; Pred. No. 2e-
Matches 67; Conservative 0; Mismatches
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AI343968.1 GI:4081174
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Unpublished (1997)
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                                                                                                                                    / lab nose="loguer" |
// clone lib="L7N800102" |
// clone lib="L7N800102" |
// clone lib="L7N800102" |
// clote="Organ: Liver; Vector: pcNS-D2; Site 1: EcoRI;
// site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (RAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
ECORI site by treatment of T4 RNA ligase and the first
ECORI site by treatment of T4 RNA ligase and the first
strand cDNA was sputhesized from oligo dr-selected mENA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
ECORI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
competent cells E. coli Toplüf' by electroporation of
the cDNA libraries constructed by this method are
full-length enriched cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakate, R., Osada, N., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N., Yanagi, S., Suto, Y., Hashimoto, K. and Hirai, M. Analyais of 5'-end sequences of chimpanzee cDNAs Genome Res. 13 (5), 1022-1026 (2003)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
1 (bases 1 to 409)
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The University of Tokyo, Graduate School of Frontier Sciences
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan
Tel: 81-4-7136-3688
Fax: 81-4-7136-3687
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Location/Qualifiers
                                                                                                                             'lab_host="Top10F
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-romail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
Tissue Procurement: Ilan Kirsch, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 586 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
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Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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DB 9; Length 409; 2e-20;
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modified polylinker: Site_1: Not I: Site_2: Eco RI;
modified polylinker: Site_1: Not II: Site_2: Eco RI;
plasmid nonA from the normalized library NoI CGAP Co10 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 10F7416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
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Seq primer: -400P from Gibco
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1 (bases 1 to 472)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                          GGGCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGGCT
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Contact: Robert Strausherg, Ph.D.
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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100.0%; Pred. No. 2e-20;
tive 0; Mismatches 0; Indels
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Homo sapiens"
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AI761519.1 GI:5177186
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Best Local Similarity 100.0
Matches 67; Conservative
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Unpublished (1997)
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1 (bases 1 to 479)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordates; Catarrhini; Hominidae; Pan.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 479)
Sakate, R., Osada, M., Hida, M., Sugano, S., Hayasaka, I., Shimohira, N., Yanagi, S., Suto, Y., Hadhimoto, K. and Hirai, M.
Analysis of 5'-end sequences of chimpanzee cDNAs
Genome Res. 13 (5), 1022-1026 (2003)
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  EST 08-MAY-2003
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479 bp mRNA linear EST 08-MAY-2AJ298317 male adult skin, full-length enriched chimpanzee cDNA library Pan troglodytes verus cDNA clone PstA5634 5' similar to human Refseq mRNA NM_002773, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Integrated Biosciences
The University of Tokyo, Graduate School of Frontier Sciences
5-1-5 Kashiwanoha, Kashiwa, Chiba 277-8562, Japan
Tel: 81-4-7136-3689
Fax: 81-4-7136-3687
Fax: 81-4-7136-3687
Fax: 91-4-7136-367
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/dessue_type="adult"
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/clore_lib="male_adult skin, full-length_enriched
chimpanzee_cDNA_library"
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AGENCOURT 13621004 NIH MGC_148 Homo sapiens cDNA clone
IMAGE:30331484 5', mRNA sequence.
CB996389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 9; hen.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.1%; Score 67; DB Best Local Similarity 100.0%; Pred. No. 2e-Matches 67; Conservative 0; Mismatches
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Pan troglodytes verus
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213 Greecen 219
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                                                                                                                                                                                                                                                                                                         M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayd by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@almage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF063417 10 CGAP CO16 Homo sapiens CDNA clone IMAGE:3323178 3' similar to SW:PSSE_HUMAN Q16651 PROSTASIN PRECURSOR ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help and advice from Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM346 row: p column: 21

High quality sequence stop: 478.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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0
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100.0%; Pred. No. 2e-20;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                       clone="IMAGE:30331484"
                                                                                                                                                                                                                                                           /mol_type="mRNA"
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BF063417.1 GI:10822327
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Unpublished (1997)
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Best Local Similarity 100.
Matches 67; Conservative
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BF063417
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/clone libe NCI CGAP CO16"
/note=Torgan: Colon; Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Bco RI; plasmid DNA from the normalized library NCI CGAP CO10 was prepared, and se circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1143551).
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                                                                                                                           /tissue type="colon tumor, RER+"
| Jab host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 25, 2004, 14:35:31 Job time : 2787 secs
1. .492
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Best Local Similarity 100.
Matches 67; Conservative
        source
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 22
LENGTH: 610
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                                                                                                                                 1 gggcccttgtcctgggccat......ggggttctgatggggcctcc 1102
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1. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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5. /cgn2_6/ptodata/2/ina/FOTUS_COMB.seq:*

5. /cgn2_6/ptodata/2/ina/FOTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-380-116-29

US-09-386-642-8

US-09-200-056-120

US-09-020-056-120

US-09-439-313-120

US-09-439-313-120

US-09-435-616A-120

US-09-159-812-120

US-09-159-812-120

US-09-159-812-120

US-09-115-453-120

US-09-685-166A-839

US-09-685-166A-839

US-09-681-1668-839

US-09-681-1668-839
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US-09-020-956-175
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RESULT 2
US-09-280-116-28/c
US-09-280-116-28/c
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Sequence 28, Application US/09280116A
Sequence 28, Application US/09280116A
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 266
SEQ ID NO 28
LENGTHARE: Patentin Ver. 2.0
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Robison, Keith E.
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
                         1175, App
126, App
127, App
128, App
225, App
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Sequence 175,
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100.0%; Pred. No. 0.082;
:ive 0; Mismatches 0
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US-09-030-607-175
US-09-332-616A-175
US-09-322-149A-175
US-09-159-812-175
US-09-685-166A-175
US-09-685-166A-175
US-09-685-166A-175
US-09-685-166A-175
US-09-685-166A-175
US-09-484-921-1
US-09-494-921-28
US-09-494-921-29
US-09-494-921-25
US-09-494-921-25
US-09-494-921-25
US-09-493-113-225
US-09-332-149A-225
US-09-332-149A-225
US-09-332-149A-225
US-09-332-149A-225
US-09-332-149A-225
US-09-332-149A-225
US-09-332-149A-225
US-09-685-166A-225
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LOCATION: (1). (610)
OTHER INFORMATION: n = a, t, C,
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 24; Conserv
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GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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EDNESS: single
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STATE: WA
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          US-09-386-642-7
                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Sequence 29, Application US/09280116A
Sequence 29, Application US/09280116A
Sequence 29, Application US/09280116A
GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
FILE REFERENCE: 5800-24, 035800/176965
CURRENT PILLIAGION NUMBER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARR: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 340
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                                                                                                    Gaps
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                                                           Length 340;
                                                                                                    0; Indels
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Sequence 8, Application US/09386642

Sequence 8, Application US/09386642

GENERAL INFORMATION:

APPLICANT 01, Jenson

APPLICANT 01, Jenson

APPLICANT 01, Jenson

TITLE OF INVENTION: Zymogen Activation System

TITLE OF INVENTION: Zymogen Activation System

TITLE OF INVENTION: 290909 Activation System

CURRENT APPLICATION NUMBER: US/09/386,642

CURRENT FILING DATE: 1999-08-31

WUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 1142
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; CTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-29
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Pred. No. 0.69;
0; Mismatches
OTHER INFORMATION: trypsin-like serine proteases
                                                        ch 2.1%; Score 23; DB 4;
1. Similarity 100.0%; Pred. No. 0.25;
23; Conservative 0; Mismatches
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100.0%; Pre
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Matches 22; Conservative
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ORGANISM: Homo sapiens
                                                                                   Best Local Similarity
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US-09-280-116-29/c
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US-09-386-642-8
          ; OTHER INFORM
US-09-280-116-28
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Sequence 120, Application US/09020956
Sequence 120, Application US/09020956
Sequence 120, Application US/09020956
GENERAL INFORMATION:
APPLICANT: Xu, diangelum
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: G100 Columbia Center, 701 Fifth Avenue
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0.69;
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PAPEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
                                             GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.0%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.6 Matches 22; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 90 base pairs
                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1169
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Sequence 7, Application US/09386642 Patent No. 6420157
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Mitcham, Gennifer Lynn
APPLICANT: Mitcham, Gennifer Lynn
APPLICANT: Mitcham, GennoUns For ImmunoTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT RPLICATION UNMERR: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 90
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                                            APPLICANT: Retter, Mark APPLICANT: Solk, John APPLICANT: Solk, John APPLICANT: Solk, John APPLICANT: Solk, John TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPRENDED: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: S75
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 90
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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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1.9%; Score 21; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-352-616A-120/c
; Sequence 120, Application US/09352616A
; Patent No. 6395278
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LOCATION: (1)...(90)
OTHER INFORMATION: n = A,T,C or G
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; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-120
  Kalos, Michael
                               Fanger, Gary
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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US-09-232-149A-120/c
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 224
CORRESPONDENCS DESCRIPTIONS
ADDRESPENSES: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
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                               1.9%; Score 21; DB 3; Length 90;
100.0%; Pred. No. 2.2;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
STATE:
WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
TITING DATE: 25-FEB-1998
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100.0%; Pred. No. 2.2;
:ive 0; Mismatches
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NAME: Maki, David J.
REGISTRATION NUMBER: 21,392
REFERENCE DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 120:
INFORMATION FOR SEQ ID NO: 120:
LENGTH: 90 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 120, Application US/09439313
Patent No. 6329505
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
                                                                                                                                  739 GGTGACTCTGGGGGGCCCCTG 759
                                                                                                                                                                                                                                                                                            Sequence 120, Application US/09030607
Patent No. 6262245
GENERAL INFORMATION:
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ORIGINAL SOURCE:

ORGANISM: Homo sapiens

US-09-030-607-120
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Matches 21; Conservative
                                       Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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US-09-020-956-120
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FEATURE:

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42721
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
CURRENT FILING DATE: 2000-10-10
SOUTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 90
                                                                                                                                                           APPLICANT: Li, Samuel
APPLICANT: Mange, Adjun
APPLICANT: Wange, Adjun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERRANCE: 210121.42717C17
FILE REPERRANCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT APPLICATION NUMBER: US/09/636,215
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FASISEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 90;
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Similarity 100.0%; Pred. No. 2.2;
21; Conservative 0; Mismatches
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; Sequence 120, Application US/09685166A
; Patent No. 6630305
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NAME/KEY: misc_feature
LOCATION: (1)...(90)
OTHER INFORMATION: n = A,T,C or G
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
                                                                                     Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
Kalos, Michael D.
                         Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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NAME/KEY: misc_feature
LOCATION: (1)...(90)
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ORGANISM: Homo sapien
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ORGANISM: Homo sapien
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Best Local Simil
Matches 21; (
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LENGTH: 90
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APPLICANT:
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APPLICANT:
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          APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT APPLICATION NUMBER: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
LENGTH: 90
LENGTH: 90
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APPLICANT: Xu, Jiangchun
APPLICANT: Millon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOUTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.9%; Score 21; DB 4; Length 90; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 21; Conservative 0; Mismatches 0; Indels
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Patent No. 6613872
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Patent No. 6620922
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(90)
; CTHER INFORMATION: n = A,T,C or G
US-09-232-149A-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (1)...(90)
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ORGANISM: Homo sapien
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US-09-159-812-120/c
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TYPE: DNA FEATURE:

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US-09-115-453-120/c

US-09-115-453-120/c

Sequence 120, Application US/09115453B

Patent No. 6657056

GENERAL INFORMATION

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMFOUNS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND

TITLE OF INVENTION: METHODS FOR THEIR USE

PILE REFERENCE: 210121.427C4

CURRENT FILING DATE: 1998-07-14

NUMBER OF SEQ ID NOS: 228

CURRENT FILING DATE: 1980-07-14

NUMBER OF SEQ ID NOS: 228

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 120

LENGTH: 90
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| Sequence 120, Application US/09688489
| Patent No. 6664377
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun C. APPLICANT: Xu, Jiangchun C. APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Damifer Lynn TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE ITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.42702 | CURRENT APPLICATION NUMBER: US/09/688,489 | CURRENT FILING DATE: 2000-10-13 | SOFTWARE: FastSEQ for Windows Version 3.0 | SEQ ID NO 120 | SE
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1.9%; Score 21; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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1.9%; Score 21; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 21; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc feature
LOCATION: (1)...(90)
CTHER INFORMATION: n = A,T,C or G
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CCATION: (1)...(90)
CTHER INFORMATION: n = A,T,C or G
US-09-115-453-120
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, OTHER INFORMATION: n = A,T,C or G US-09-685-166A-120
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Db 34 GGTGACTCTGGGGGCCCCTG 14
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Search completed: February 25, 2004, 14:37:33 Job time : 111 secs

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OM nucleic - nucleic search, using sw model

Run on:

Pebruary 25, 2004, 13:49:01 ; Search time 454 Seconds
(without alignments)
8499.586 Million cell updates/sec

1 gggcccttgtcctgggccat......ggggttctgatggggcctcc 1102 US-10-037-417-45 1102 Title: Perfect score: Sequence:

0.09 OLIGO_NUC Gapop_60.0 , Gapext Scoring table:

2308684 segs, 1750822206 residues Searched:

0 Word size :

4617368 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

| cgn2_6/ptodata1/pubpna/USO7_PUBCOMB.Beg:*
| cgn2_6/ptodata1/pubpna/PCT_NEW_PUB.seg:*
| cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seg:*
| cgn2_6/ptodata1/pubpna/USO6_PUBCOMB.seg:*
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| cgn2_6/ptodata1/pubpna/DSO7_NEW_PUB.seg:*
| cgn2_6/ptodata1/pubpna/DSO8_PUBCOMB.seg:*
| cgn2_6/ptodata1/pubpna/USO8_PUBCOMB.seg:*
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| cgn2_6/ptodata1/pubpna/USO08_PUBCOMB.seg:*
| cgn2_6/ptodata1/pubpna/USO08_PUBCOMB.seg:* Published Applications NA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 52, Appl	Sequence 10, Appl	Sequence 21306, A	Sequence 7606, Ap	Sequence 85, Appl	Seguence 447, App	Sequence 29, Appl	Sequence 1, Appli	Sequence 2214, Ap	Sequence 141, App	Seguence 261, App	Sequence 931, App		Sequence 931, App	Sequence 31, Appl
ID	US-09-888-615-52	US-10-221-097-10	US-10-029-386-21306	US-10-029-386-7606	US-10-176-847-85	US-10-101-510-447	US-10-042-865-29	US-09-948-094-1	US-09-880-107-2214	US-09-967-768A-141	US-10-097-340-261	US-09-922-217-931	US-09-833-263-931	US-10-025-380-931	US-10-042-865-31
DB		14	14	14	14	14	12	6	σ	σ	14	σ	Φ	13	12
f Nuery Match Length DB	2457	768	315	543	1733	3382	1726	1834	1834	1834	1834	596	596	596	1161
Query Match	65.0	12.3	6.1	6.1	6.1	6.1	4.8	4.8	4.8	4.8	4.8	4.6	4.6	4.6	4.4
Score	716	135	67	67	67	67	53	53	53	53	53	51	51	51	49
Result No.		2	т О	Ω 4,	ស	9	7	80	σ	10	11	c 12	c 13	c 14	15

Sequence 208, App Sequence 710, App Sequence 288, App	58,	377	Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli		4, <i>P</i> 1668,	Sequence 81, Appl Sequence 81, Appl		Sequence 19, Appl Sequence 33, Appl	34,	68,	29	e 19	, נ מינ	sequence 23, Appl
9 US-09-925-301-208 9 US-09-764-864-710 9 US-09-764-864-288	09-879-792-1 09-888-615-58	S-10-06 S-10-06 S-10-31	9 US-09-912-559-1 9 US-09-912-559-2 15 US-10-391-215-1	0-391-21 0-391-21	15 US-10-391-215-4 9 US-09-880-107-1668	14 US-10-131-409-81 15 US-10-150-811-81	14 US-10-240-730-1 14 US-10-131-409-19	15 US-10-150-811-19 12 US-10-042-865-33	12 US-10-042-865-34 14 US-10-240-730-3	9 US-09-764-898-68	US-10-399	US-10-156-214A	US-09-888-615-	12 US-10-399-645-23
1668 1005 1282	138	1169	1683 1683 1683	1683	1683 3008	174	296 870	870 882	882	1375	2255	3316	3387	37,11
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ALIGNMENTS

APPLICANT: WHYTE, DAVID
APPLICANT: CRENEDEEL, SEAN
APPLICANT: CRENEDEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: SUDARSANAM, SUCRA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERENCE: 038602/1214
CURRENT APPLICATION NUMBER: 05/214,047
FILMS PRIOR APPLICATION NUMBER: 60/214,047
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SEQ ID NO 52
SEQ ID NO 52 Sequence 52, Application US/0988615 Patent No. US20020064856A1 GENERAL INFORMATION: APPLICANT: PLOWMAN, GREGORY TYPE: DNA ORGANISM: Homo sapiens RESULT 1 US-09-888-615-52 LENGTH: 2457 US-09-888-615-52

ö 128 ACTGCGGGCCCTGAGCCCTCGGCCCCGCATCGTGGGGGGGCTCAAACGCGCAGCCGGGCA 187 169 110 ACTGCGGGCCCCTGAGCCCTCGGCCCGCATCGTGGGGGGCTCAAACGCGCAGCCGGGCA Gaps 0, DB 9; Length 2457; Indels 2, Score 716; DB Pred. No. 0; 0; Mismatches Query Match 65.0%; Best Local Similarity 99.8%; Matches 816; Conservative g à

188 CCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGTGGCCACATCTGCGGGGGTCCCCTCA 247 229 248 TCGCCCCCTCCTGGGTCCTCTCCGCTGCTCTTTCATGACGAATGGGACGTTGGAGC 307 Ω ð

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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 315
                     SEQ ID NO 10
LENGTH: 768
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                                                                            350 CGCACACCCGCCCAGAGAGCCGCCATCGTGCTGCCGCCCAACTACAGCCAAGTGGAGCTGG 409
                                                                                                                                                                                                                        410 écéccéaccidédecergéradeserrédecerédecesécéadeserrédecerédes 469
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                                                                                                                                                                                                                                                                                607
                                                        CCGCGGCCGAGTGGTCGGTACTGCTGGGGCGTGCACTCCCAGGACGGGCCCTGGACGGCG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGGGGAGACGTCCAGGAGGCAGATCCTCTGCCTCTCCCCTGGGTGCTACAGGAAGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          848 CIGCIGIGGCIACCIAIGAGGCAIGGAIACGGGAGCAGGIGAIGGGIICAGAGCCIGGGC
   ACCICACICICCAGAIATIGCCAGGGAIGCIGIGCIGGCIACCCAGAGGGCCGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACACCTGCCAGGGTGACTCTGGGGGCCCCTGGTCTGTGAGGAAAGGCGGCCGCTGGTTCC
                                                                                                                          CGCACACCCCCCCATGCCCCCATCGTGCCCGCCCAACTACAGCCAAGTGGAGCTGG
                                                                                                                                                                                            CTGCCTTTCCCACCCAGCCCCAGAAGACCCCAGTCAGAT 945
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US-10-221-097-10
Sequence 10, Application US/10221097
Publication No. US20030144476A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
PRICANT: APPLICATION NUMBER: US/10/221,097
CURRENT FILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR PILING DATE: 2000-03-05
PRIOR PILING DATE: 2000-03-05
PRIOR APPLICATION NUMBER: 60/187,107
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-13
PRIOR PILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-03-13
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANZEL, David R.
APPLICANT: HANZEL, DAVID R.
TITLE OF INVENTION: HURAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR UTITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                                                                                                                                        217 GGAGGIGGCCACAICIGCGGGGGCICCCICAICGCCCCCTCCIGGGICCICTCCGCIGCI
                                                                                                                                                                                                                                                                                                                                                                                            61 GGAGGTGGCCACATCTGCGGGGGGTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTCCT
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OTHER INFORMATION: MAP TO CHRI6.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN ENTAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: WITH: 9114779472, EVALUE 0.000e+00
OTHER INFORMATION: SWISSPROT HIT: Q1651, EVALUE 0.000e+00
US-10-029-386-21306
                                                                                                        Query Match
12.3%; Score 135; DB 14; Length 768;
Best Local Similarity 100.0%; Pred. No. 6e-59;
Matches 135; Conservative 0; Mismatches 0; Indels
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6.1%; Score 67; DB 14; Length 315;
Best Local Similarity 100.0%; Pred. No. 5.5e-24;
Matches 67; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 CACTGTTTCATGACG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACTGTTTCATGACG 291
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TYPE: DNA
CORGANISM: Homo sapiens
US-10-221-097-10
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212 dedecerriereceredececaradecedadadeserecreseceredecadadecen 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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0
                        Sequence 447, Application US/10101510
; Sequence 447, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; TITLE OF INVENTION: UNMERR: US/10/101,510
; CURRENT APPLICATION NUMBER: 05/206,947
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2001-03-20
; PRIOR FILING DATE: 2010-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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100.0%; Pred. No. 4e-24;
tive 0; Mismatches 0.
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CURRENT APPLICATION NUMBER: US/10/042,865
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
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Grosse, William M
Alsobrock II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
Malyankar, Uriel M
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
APPLICANT: Casman, Stacie J
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly
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Miller, Charles E
Guo, Xiaojia
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Gunther, Erik
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                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-101-510-447
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     272 GTGGCCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GTGGCCA 67
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: Penn, Barid R.
APPLICANT: Rank, David R.
APPLICANT: Barid Javid R.
APPLICANT: Barid Javid R.
APPLICANT: Barid Javid R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICANTON NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 7606
LENGTH: 543
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                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO CHRI6.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN BAZIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
OTHER INFORMATION: WILL ST HUMAN HIT: Q11421281, SVALUE 7.00e-04
OTHER INFORMATION: NT HIT: U33446.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67; DB 14; Length 1733;
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Best Local Similarity 100.
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
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SENERAL INFORMATION:
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US-10-029-386-7606
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                  TYPE: DNA
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APPLICANT: Wok, Samuel
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE REFERENCE: 81994/28423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 1834
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J Sequence 2214, Application US/09880107

J Sequence 2214, Application US/09880107

J PATENT NO. US20020142981A1

J APPLICANT: Wockley, Joseph G.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WS/09/880,107

CURRENT APPLICAND NUMBER: US/09/880,107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1834;
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Best Local Similarity 100.0%; Pred. No. 6.7e-17;
Matches 53; Conservative 0; Mismatches 0; Indels
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Patent No. US20020090625A1
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. c...
0; Mismatches
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-03-09
PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR APPLICATION NUMBER: 60/284,704
PRIOR PILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
SOFTWARE: PATENTIN Ver. 2.1
LENGTH: 1726
                                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Conservative
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; LOCATION: (229)..(1260)
US-09-948-094-1
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-10-042-865-29
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Best Local Similarity
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US-09-948-094-1
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Sequence 14.1, Application US/09967768A

| Sequence 14.1, Application US/09967768A
| Patent No. US20020150877A1
| GENERAL INFORMATION:
| APPLICANT: Augustus, Meena
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatus
| TITLE OF INVENTION: Sets
| TITLE OF 
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US-09-880-107-2214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4.8%; Score 53; DB 9; Length 1834; 100.0%; Pred. No. 6.7e-17; tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 6.7e-1
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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 2214
LENGTH: 1834
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: JOHN MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Gordon B. MILLS
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                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
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Matches 53; Conserv
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Best Local Similarity
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US-09-967-768A-141
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US-10-097-340-261
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51

US-09-922-217-931

APPLICANT:

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Sequence 931, Application US/09833263

Facent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Wang, Alin

APPLICANT: Clapper, Jonathan D.

APPLICANT: Clapper, John A.

TITLE OF INVENTION: CMCMPOUNDS FOR IMMUNOTHERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFRENCE: 21012.1.471C12

CURRENT FILING DATE: 2001.4-10

NUMBER OF SEQ ID NOS: 1093

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 596
                                                                                                                                                                                                                      589 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCCTGGGCAG 539
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CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
                                                                                                                                                                  1 GGGCCCTTGTCCTGGGCCATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCCAG
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4.6%; Score 51; DB 9; Length 596
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                            Indels
                                                      Query Match

'4.6%; Score 51; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 51; Conservative 0; Mismatches 0;
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Publication No. US20020182191A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Eodes, Michael J.
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
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; LOCATION: (1)...(596)
; CTHER INFORMATION: n = A,T,C or G
US-09-833-263-931
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
Clapper, Jonathan D.
Skeiky, Yasir A. W.
Fanger, Gary R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-025-380-931/c
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                              APPLICANT: Xunei ZHAO
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT PLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
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APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Smith, Carole Lynn
APPLICANT: Ming, Gardon E.
APPLICANT: Wang, Aljun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FASESEQ for Mindows Verbion 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.8%; Score 53; DB 14; Length 1834; Best Local Similarity 100.0%; Pred. No. 6.7e-17; Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 363
SOFTWARER PESTSEQ for Windows Version 4.0
SEQ ID NO 261
LENGTH: 1834
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Patent No. US20020076414A1
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Robert C. BAST, Jr.
Karen LU
                                             Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-097-340-261
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-922-217-931/c
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LENGTH: 596
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APPLICANT:
APPLICANT:
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δ QQ ö

Gaps

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TYPE: DNA

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SECTION SET PRESENCE FOR WINDOWS VERSION 4.0

SECTION 5.30

TARGETH SES

TARGETH SE
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Search completed: February 25, 2004, 15:44:57 Job time : 457 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 25, 2004, 14:35:42; Search time 100 Seconds (without alignments) 1008.695 Million cell updates/sec Run on:

US-10-037-417-46

1953 Title: Perfect score:

1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357 Sequence:

1586107 segs, 282547505 residues Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table: Searched:

1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1090s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003as:*
geneseqp2003bs:* A_Geneseq_29Jan04:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abb09524 Human pro	Abb09523 Human pro	Abb98135 Human PMM	Aau82753 Amino aci				_	Human	Amino	Human	Human	Human	Human	Abg72018 Mouse cha	Human			Novel			_		Aag67514 Amino aci	Abb07284 Human pro
SUMMARIES	ID	ABB09524	ABB09523	ABB98135	AAU82753	AAM93568	AAU75082	ABG04853	ABG96402	AAU78547	ABB07285	ABJ37067	ADD47565	ADD47561	ABB98415	ABG72018	ABB98416	ABP61011	ABB07286	ABP61010	ABG91414	AAU00467	AAU74748	AAE14348	AAG67514	ABB07284
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o lf	Query Match	100.0	96.0	77.1	77.1	61.5	49.7	41.2	35.3	35.3	35.3	35.3	35.3	35.3	33.0	32.1	31.3				30.2	30	7	29.8	29.5	29.4
	Score	1953	1874	1505	1505	1202	970	804.5	069	069	069	069	069	9	645	627.5	612	593.5	590	590	590	590	582.5	582	575.5	~
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pol	epi	aci	clon	PRO	pro	gen	alb	μnq	PRO	PRO	sec	sec	ser	sec	hum	PRO	PRO	sapi	hum	
Human	Human	Amino	HTRM C	Human	Human	Human	Human	Novel	Human	Human	Novel	Human	Human	Human	Novel	Human	Human	ношон в	Novel	
Aam41174	Aau75907	Aaw77304	Aay73388	Aau12282	Aab73945	Aae03821	Abg64545	Abo17726	Abu80980	Abu66680	Abu59761	Abo24951	Abg73394	Abu66956	Ada45741	Ada76172	Ada18822	Ada61445	Adb19230	
AAM41174	AAU75907	AAW77304	AAY73388	AAU12282	AAB73945	AAE03821	ABG64545	AB017726	ABU80980	ABU66680	ABU59761	AB024951	ABG73394	ABU66956	ADA45741	ADA76172	ADA18822	ADA61445	ADB19230	
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328	389	297	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	
29.1	29.0	29.0	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	28.8	
568.5	567	266	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	563	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Human, NOVX; neurological disorder; Alzheimer's disease;

Humtington's disease; Parkinson's disease; pain; behavioural disorder;

M Huntington's disease; Parkinson's disease; pain; behavioural disorder;

M addiction; tuberous sclarosis; nathma; arthritis; diabetes;

M thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

M thyroiditis; nacontinence; psoriasis; scleroderma; alopecia;

M pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

M polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

M polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

M metabolic pathway regulation disorder; cytostatic; neuroprotective;

M metabolic pathway regulation disorder; cytostatic; neuroprotective;

M dermatological; antibacterial; antiarthritic; hepatocropic; neurogenesis;

M differentiation; proliferation; motility; hematopoiesis; wound healing;

M andiogenesis; forensic biology; transgenic animal; drug screening;

M gene therapy; NOV14b; prostatin precursor-like.
                                                                                                                                        Human prostatin precursor-like NOV14b protein, SEQ ID NO:46.
                                    ABB09524 standard; protein; 357 AA.
                                                                                                          (first entry)
                                                                                                            01-NOV-2002
                                                                         ABB09524;
RESULT 1
ABB09524
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Homo sapiens.

WO200253742-A2.

11-JUL-2002.

08-JAN-2001; 2001US-0260360P. 28-FBE-2001; 2001US-0272411P. 02-MAR-2001; 2001US-0272817P. 05-JUL-2001; 2001US-0305060P. 12-JUL-2001; 2001US-0305060P. 10-SEP-2001; 2001US-0318405P. 07-JAN-2002; 2002WO-US000375. 2001US-0260360P. 2001US-0272411P. 05-JAN-2001; 2001US-0260018P.

(CURA-) CURAGEN CORP.

2002US-00037417

12-SEP-2001; 04-JAN-2002;

Li L; Tchernev VT, Liu X, Spytek KA; Lepley DM, Burgess CE, Vernet CAM, Kekuda R, Alsobrook JP, ' Patturajan M, Grosse WM,

Ellerman K, Malyankar U; , Guo X, Shenoy S, Anderson D; Guo X, Sh , Eisen A; Sciore P, Elle), Boldog F, Gu tJ, Miller CE, Edinger S, Sci M, Stone D, B 1, Taupier RJ, Padigaru M, Gorman L, Rothenberg

2002-583619/62 WPI; 2002-583619 N-PSDB; ABQ93902

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

Claim 1c; Page 143; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleotides across encoding them (ABQ03879-ABQ03902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX nucleotides are useful in the manufacture of a medicament for treating such associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 NOVX proteins, based on their homology to known proteins. Various disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), ce.g., allergies and autoimmune diseases), myasthenia gravis, cancers (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritisy, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, incomninence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, incomninence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocarine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NOVX mucleic acids and polypeptides may be used to identification of small molecules that modulate or inhibit processes such contining to a NOVX protein, and are also useful as targets for the binds to a NOVX protein, and are also useful as targets for the cardiomyopanic, and continence of prinmers or probes for foremaic but type and are useful as a source of prinmers or probes for foremaic but of comprising NOVX nucleic acids are useful for producing non-human compressing NOVX nucleic acids are useful for studying the function and for infinity or all protein and for infinity and or all protein and for infinity and all protein and are also useful per producing activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents the prostatin precursor like protein NOV14b

Sequence 357 AA;

120 9 9 1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW 1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW Gaps ., 100.0%; Score 1953; DB 5; Length 357; 100.0%; Pred. No. 5.2e-146; ive 0; Mismatches 0; Indels 0; Matches 357; Conservative Similarity Query Match Local В ά 8

QVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTR 120 QVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTR 61 61

> d à qq ð Ω ò g

121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD VQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ 181 VOEADPLPLPWVLQEVELKLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ 181

121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD

GDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFF 300

241

GDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFP

357 301 TQPQKTQSDCLHQTAFLDSARILLRPLSHISVGVSTGTKSLVJPWLSPHSLLGLWGF Dp à

RESULT 2 ABB09523

Z ABB09523 standard; protein; 344

ABB09523;

(first entry) 01-NOV-2002 Human prostatin precursor-like NOV14a protein, SEQ ID NO:44.

Huntington's disease; Parkinson's disease; pain, behavioural disorder;

W Huntington's disease; Parkinson's disease; pain, behavioural disorder;

W addiction, tuberous sclerosis; cancer; immune disorder; allergy;

Autoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

W thyroiditis; cardiovascular disease; hypertension; reproductive disorder;

W endometriosis; incontinence; psoriasis; scleroderma; alopecia; ulcer;

W pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;

W polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;

W atherosclerosis; cell signal processing-related disorder;

W metabolic pathway regulation disorder; cytostatic; neuroprotective;

W metabolic pathway regulation disorder; cytostatic, neuroprotective;

W metabolic pathway regulation disorder; phepatotropic; neurogenesis;

W defractological; antibacterial; antiarthitic; hepatotropic; neurogenesis;

W differentiation; proliferation; moullity; heematopoiesis; wound healing;

M angiogenesis; forensic biology; transgenic animal; drug screening;

W gene therapy; NOV14a; prostatin precursor-like; chromosome 16. Human; NOVX; neurological disorder; Alzheimer's disease;

MO200253742-A2.

11-JUL-2002.

07-JAN-2002; 2002WO-US000375.

08-JNN-2001; 2001US-0260360P. 28-FBB-2001; 2001US-0272411P. 02-MAR-2001; 2001US-0272817P. 05-UUL-2001; 2001US-0303231P. 12-UUL-2001; 2001US-0305660P. 10-SEP-2001; 2001US-0318405P. 05-JAN-2001; 2001US-0260018P

2002US-00037417 04-JAN-2002;

(CURA-) CURAGEN CORP.

į, Tchernev VI, Liu X, Spytek KA; Lepley DM, Burgess CE, Vernet CAM, Li iore P, Ellerman K, Malyankar U; Boldog F, Guo X, Shenoy S, Anderson D; DM, Ellerman K, Mar, Λιο X, Shenoy S, Patturajan M, Grosse WM, Lepley DM, Gorman L, Rdinger S, Scioce P, Ella Rochtenberg M, Stone D, Boldog F, G Padigaru M, Taupier RJ, Miller CE, Alsobrook JP, Kekuda R,

2002-583619/62.

N-PSDB; ABQ93901

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

> 180 180 240 240 300

Claim 1c; Page 142; 323pp; English

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and mucleic acids encoding them (ABG93879-ABQ93902). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24

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(e.g., allergies and autoimmune diseases), mysethenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, incontinence, psoriasis, scleroderma, alopecia, ulcers, panoreatitis, cirrhosis, glomerular endotheliosis, polycystic kidney disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, attheosocierosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NoWX nucleic acids and polyceptides may be used to identify cellular receptors or downstream effectors which binds to a NoWX protein, and are also useful as targets for the identification of small molecules that modulate or inhibit processes such as neurogenesis, cell differentiation, cell motility, cellular profileration, haemacopoiesis, wound healing and angiogenesis. NoWX nucleic acid sequences can be used to identify a cell or tissue type and nucleic acid sequences can be used to identify a cell or issue type and nucleic acid sequences can be used to identify a cell or issue type and nucleic acid sequences can be used to identify a cell or issue type and nucleic acid sequences can be used to identify as the modulate or inhibit processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful as a source of primers or probes for forensic biology and for identifying and coloning NOVX homologues in other cell types. Cells comprising NOVX nucleic acids are useful for producing non-human transgenic animals which are useful for studying the function and activity of NOVX proteins and for identifying and evaluating modulators of NOVX activity. The present sequence represents the prostatin precursor like protein NOV14a. The gene encoding NOV14a is located on chromosome
NOVX proteins, based on their homology to known proteins. Various disorders are associated with NOVX proteins including neurological disorders (e.g., Alzaheiner's, Huntington's and Parkinson's diseases), pain, behavioural disorders, addiction, tuberous sclerosis, cancers (e.g., colorectal cancer, leukaemia and osteosarcoma), immune disorders
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                                                                                     9
                                                                                                                    1 MAQKGVIGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW
                                                                                                                                                                                                181 VQEADPLPLPWVLQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFP
                                                                                   1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPW
                                                                                                                                                                                                                                                     121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD
                                                                                                                                                                                                                                                                                 121 AVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGD
                                                                                                                                                                                                                                                                                                                                      VQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQ
                                                                                                                                                                    61 QVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTR
                                           Gaps
                                           ..
0
  Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOKTOSDCLHQTAFLDSARILLRPLSHISVGVSTGTKSLVLP 344
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96.0%; Score 1874; DB 5; Length 3 100.0%; Pred. No. 8.6e-140; ive 0; Mismatches 0; Indels
                                         Matches 344; Conservative
                     Local Similarity
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Human; PMPM; protein modification and maintenance molecule;
anticonvulsant; neuroprotective; notroppic; vytostatic; antipsoriatic;
antiasthmatic; dermatological; antidiabetic; antiparkinsonian;
antianammic; antiinflammatory; antiulcer; antianginal; cardiant;
                Ź
                                                                                                             Human PMMM Incyte ID 2751509CD1.
             ABB98135 standard; protein; 818
                                                                             (first entry)
                                                                             17-0CT-2002
                                             ABB98135;
ABB98135
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antibacterial; fungicide; gastrointestinal; antidiarrheic; laxative; haemostatic; anti-HIV; thrombolytic; anticoagulant; gynaecological; cardiovascular; antiarteriosclerotic; hypotemsive, vasotropic; antitheumatic; lamunosuppressive; antiallergic; antithyroid; nephrotropic; antigout; thyromimetic; antiarthritic; uropathic; ophthalmological; antigout; thyromimetic; antiarthritic; uropathic; antisoborhaic; antidepressant; neuroleptic; antinfertility; andicory; antisoborhaic; antidepressant; neuroleptic; antinfertility; antisomency; antisopical; Crohn's disease; hypertension; autoimmune; inflammatory; anemaia; cell proliferative; developmental; epithelial; scabies; neurological; Alzhaimer's disease; reproductive; ectopic pregnancy; gene therapy; vaccine; disorder; prostasin. hepatotropic; osteopathic; antiemetic; antipyretic; virucide;

Homo sapiens

WO200246383-A2.

13-JUN-2002

05-DEC-2001; 2001WO-US046964.

08-DEC-2000; 2000US-0254399P

21-DEC-2000; 2000US-0257803P. 05-JAN-2001; 2001US-0260110P. 19-JAN-2001; 2001US-0262851P.

25-JAN-2001; 2001US-0264623P.

(INCY-) INCYTE GENOMICS INC.

Griffin JA, Swarnakar A; Au-Young J, Elliott VS; , Lu DAM, Lee EA; MG, Khan FA; Baughn MR, Griff Gandhi AR, Au-3 ', Warren BA, Lu ane AM, Yao MG, Azimzai Y, Kallick DA, Baughn Bwalia NK, Hafalia AJA, Gandhi Lr J, Thangavelu K, Lu Y, Warre.ey CM, Arvizu C, Delegeane AM, Yue H, Azim Lal PG, Wal Ramkumar J, Tribouley

Sanjanwala MM;

WPI; 2002-519664/55. N-PSDB; ABQ75956. New isolated Protein Modification and Maintenance polypeptides, for diagnosis, and treatment of e.g. gastrointestinal disorders

Claim 1 (a); Page 174-176; 200pp; English.

The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptide. Polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMM. These include gastrointestinal disorders (e.g. Crohm's disease), cardiovascular disorders (e.g. unaemia), cell proliferative disorders, developmental disorders (e.g. anaemia), cell proliferative disorders, developmental disorders, epithalial disorders reproductive disorders (e.g. attainer's disease) reproductive disorders (e.g. ectopic pregnancy), and in gene therapy or a vaccine for such diseases. They may also be used in the assessment of the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules. The found to have homology with rat prostasin

Sequence 818 AA;

6 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP Gaps 0; Length 818; 77.1%; Score 1505; DB 5; Length 8 ilarity 100.0%; Pred. No. 3.2e-110; Conservative 0; Mismatches 0; Indels Best Local Similarity Matches 272; Conserv Query Match à g 98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP

ö 엄 $\dot{\delta}$

157

158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN 217

ó

Gaps

.; 0

Length 818; Indels 157 157 217 217 277 277

97

38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP

.77.1%; Score 1505; DB 5; I 100.0%; Pred. No. 3.2e-110; tive 0; Mismatches 0;

Conservative

Similarity

Query Match Best Local Simil Matches 272; C

8

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38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWINGTLEP

98 AAEWSVILGVHSQDGPIDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVNP

98 AAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADIALIRIASPASLGPAVWP

LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT

VCLPRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN

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Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; enzyme.
VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGBATCQCLXSQPGPFN 217
                                           218 LTLØILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT
                               LILQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT
                                                                                                                                                                                                          Amino acid sequence of novel human protease #52.
                                                                          AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                         278 AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                 AAU82753 standard; protein; 818 AA.
                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001; 2001WO-US020171.
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                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                            WO200200860-A2
                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                  218
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218 218

158

AVATYEAMIREQVMGSEPGPAFPTQPQKTQSD 309 AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309

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AAM93568 standard; protein; 766

AAM93568

RESULT

Human; full length cDNA; cDNA synthesis; oligo-capping.

07-JUL-2000; 2000EP-00114089

EP1130094-A2. Homo sapiens.

05-SEP-2001

Sudarsanam S, Manning G, Caenepeel S;

Whyte D,

Charydczak G;

Plowman G,

(SUGE-) SUGEN INC

2002-139913/18.

WPI; 2002-139913, N-PSDB; ABK31795

Claim 6; Fig 2R; 313pp; English.

99JP-00194486

08-JUL-1999;

L1-JAN-2000; 2000JP-00118774 02-MAY-2000; 2000JP-00183765

Human polypeptide, SEQ ID NO: 3347.

06-NOV-2001

AAM93568;

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for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kawai Y;
T, Koga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; SEQ ID NO 3347; 1380pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kawa T, Isogai T, Hayashi K, Ishii S,
Sugiyama T, Nagai K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in genetic manipulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-524255/58.
N-PSDB; AAK94500.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830 Primers useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wakamatsu A,
The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. inflammatory diseases), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic disorders (e.g. diabetes, obesity), inflammatory diseases (e.g. metabolic renumatoid arthritis and psoriasis), central or peripheral nervous system diseases, mayaranes, pain, sexual dysfunction, mood disorders, attention disorders, proposed disorders, encological disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. dianomal and acular degeneration. ANUS2702-AAUS2760 represent the novel
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Finers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM

human proteases of the invention

Sequence 818 AA;

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RESULT 7
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                                                                                                                           209
                                                                                                                                     121 YSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR 180
                                                                                                                                                                                                                                                                                                                                                                                                refal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease.
                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                Human, prostasin-like serine protease, cytostatic, antiatherosclerotic, virucide, osteopathic, antiinflammatory, vasotropic, neuroprotective, trypsin-like, metastasis, autoimmune lesion, atherosclerosis;
                                                                               90 MINGILEPAAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA
                                                                                                   1 MINGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA
                                                                                                                        150 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL
                                                                                                                                                                 210 YSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR
                                                              Gaps
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(62. .173
                                         Length 766;
                                                             Indels
                                                                                                                                                                                                                       270 RNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "Type I fibronectin domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "Type I fibronectin domain"
                                       Query Match 61.5%; Score 1202; DB 4; Best Local Similarity 100.0%; Pred. No. 2.5e-86; Matches 220; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Apple protein domain"
.61. .174
                                                                                                                                                                                                                                                                                                                                             Human prostasin-like serine protease protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Trypsin_ser region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Trypsin_His region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Kringle domain"
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                                                                                                                                                                                                                                                                                AAU75082 standard; protein; 178 AA.
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .177
format directly from EPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                     Query Match
Best Local Similarity
                    Sequence 766 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200198467-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                          08-MAY-2002
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This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease is useful fulid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, used as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive used to modulate enzyme activity in a disease, such as metastasis of malignant disease (CoDD), atherosclerosis, neurodegenerative disease (CoDD), atherosclerosis, neurodegenerative disease (CoDD), atherosclerosis, neurodegenerative disease (CoDD), atherosclerosis, neurodegenerative disease (CoDD), atherosclerosis, particularly viral infection. The human prostasin-like serine procease as a crivity, in particular for treating or preventing metastatic cancer. The carpentic target of decreasing human prostasin-like serine provides a ctivity, in particular for treating or preventing may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants corporosis, Paget's disease and degradation of bone implants and libid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic and libid accumulation and inhibit the progression of restenosis and anterosclerosis. The nucleic acid sequence is also useful in diagnostic diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human procession of prostasin-like serine protease sequence of the invention and inhibit accumulations in nucleic acid sequence of the invention construction of the presence of the invention and invention and inhibit accumul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                        Novel human prostasin-like serine protease polypeptide and polymucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 LGADLALIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 LIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 LIAPSWVLSAAHCFMINGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.7%; Score 970; DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #4844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; 111pp; English.
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23-JUN-2000; 2000US-0213588P.
20-MAR-2001; 2001US-0276909P:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                   WPI; 2002-114576/15.
                                                                                                                                                                                            Kiao Y, Morozov V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                            (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                     N-PSDB; ABK13565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG04853;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centification of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centification formal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 35212; 103pp; English.
                                                                                                                                                                       30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                             Tang YT;
                                                                                                                                                                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAS69040.
                                                                                  WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biodiversity.
                                           Homo sapiens.
                                                                                                                         11-OCT-2001
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153 PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQ 212
                                                                                                                                                                                                       61 PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQ 120
                                                                                                                                           9
                                                                                                         93 GTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLG
                                                                                                                             GTLEPAAEWSVLLGVESQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLG
                                                                   Gaps
                                                                     -1
                               41.2%; Score 804.5; DB 4; Length 198; 96.2%; Pred. No. 1.3e-55; ive 1; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                          PGPFNLTLQILPGMLCAGYPEGRRDTCQ-GDSGGPL 247
                                                96.2%;
                                                                     Conservative
                                                    Local Similarity
Sequence 198 AA;
                                                                   Matches 150;
                                                                                                                                                                                                                                                                                    121
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                                   Query Match
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selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the

Sequence 343 AA;

nvention

ABG96402 standard; protein; 343 AA.

ABG96402;

ABG96402 ID ABG9 XX AC ABG9 RESULT 8

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The present inversion relates to a new method involves comparing the expression level of a marker in a patient sample and the normal level of expression level of a marker in a control non-ovarian cancer sample, where the expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing cancer). The cancer markers may be used in the management and treatment cancer. The cancer as familial history of ovarian cancer. The cancer as disease or parkinson's disease, brain cancer. The cancer markers may be used in the management and treatment cancer. The cancer markers may be used in the management and treatment cancer. The cancer markers may be used in the management and treatment cancer (e.g. bacients may be used in the management and treatment cancer (e.g. bacterial or viral meningities or encephalitis), inflammations (e.g. bacterial or viral meningities or encephalitis), connective tissue disorders (e.g. ontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with the whether ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is labely to metastasize.
                                                                                                 Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granullomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new method for assessing whether a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gannavarapu M, Hoersch S, Kamatkan
Morrisey MP, Olandt PJ, Sen A, Vie
u K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 385; 481pp; English.
                                                           Human ovarian cancer marker OV80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-0324967P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325149P.
                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2002; 2002WO-US007826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC
                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lu K,
                                                                                                                                                                                                                                                                                                                                    WO200271928-A2.
                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2001;
                   11-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monahan JE,
                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meyers RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bast RC,
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Kovatis SG;), Mills GB;

Vieby PO, Kamatkar S,

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                                                                                                                                                                                                                  111 DAKVSTLKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTV 170
                                                                                                                                                                                                                                                                                   56 GTWPWQVSLHHGGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                               GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                                                                                                                              236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                               55
                                                                                                53
                                                                                                                                                                                                                                                                                                                                                                                              296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                 289 OPRVVPQTQESQPDSNLCGSHLAFSSAPAQGILRPILFIPLGLALG---LLSPWLSEH 343
                                                                                      1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                            54 GOWPWOVSITYEGVHVCGGSLVSEOWVLSAAHCFPSEHHKE---AYEVKLGAHOLDSYSE
                                                                                                                                                                                                                                                               TGWGDVQEADPLPLPWVLQEVELRLIGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing cancer or susceptibility to it, useful particularly for ovarian cancer, comprises detecting increased levels of prostatin in blood or tissue.
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prostasin; human; malignant; cancer; ovarian cancer; breast cancer; prostate cancer; lung cancer; colon cancer.
                                24;
 Length 343;
                               Indels
35.3%; Score 690; DB 5; 43.6%; Pred. No. 2.7e-46;
                               49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 34-36; 36pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2000; 2000US-0231166P
             Best Local Similarity 43.6
Matches 156; Conservative
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N-PSDB; ABK12241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mok SC, Wong K;
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Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DAKVSTIKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostasin-like enzyme; human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; gene therapy; antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human prostasin-like enzyme polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLFLGLALG---LLSPWLSEH 343
may also be applicable to breast, prostatic, lung and colonic cancers. Using the method of the invention it was shown that in ovarian cancer, the highest levels of prostatin were found in stage II disease, suggesting that this marker is suitable for early detection. The prese sequence represents the human prostasin protein used in the method of invention as a marker for early detection of cancer or susceptability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQKGVIGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
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                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                      Length 343;
                                                                                                                                                                                                                                                                                                                                   ; Score 690; DB 5; Length 34; Pred. No. 2.7e-46; 49; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                      35.3%;
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22-MAR-2001; 2001US-0277612P.
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                                                                                                                                                                                                                                                                     Sequence 343 AA;
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The invention comprises a method for assessing whether a patient is afflicted with breast cancer or ovarian cancer. The method involves the use of specific DNA markers. The method of the invention is useful in the detection and treatment of ovarian and breast cancer. Amino acid sequences ABJ37025 - ABJ37080 represent human breast/ovarian cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAKVSTIKDIIPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 KDACÓGDSGGPLSCPVEGLWYLTGÍVSWGDACGARNRÞGVYTLASSYASWÍQSKV--TEL 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                               Determining the presence of breast cancer in an individual, involves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.3%; Score 690; DB 6; Length 34:43.6%; Pred. No. 2.7e-46; ive 49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 193~194; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           using specific polynucleotide markers.
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                                                                         21-JUN-2002; 2002WO-US019773.
                                                                                                                         21-JUN-2001; 2001US-0300159P.
27-JUN-2001; 2001US-0301351P.
                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABT31936.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           related proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
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                      03-JAN-2003
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                                                                                    The invention relates to human prostasin-like enzyme polypeptides and polynucleotides. The enzyme can be expressed by standard recombinant methodology. The polypeptide, polynucleotide and modulators are useful for treating diseases like metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atheroscilerosis, neurodegenerative disease and pathogenic infection, particularly viral infection. The prostasin-like enzyme gene provides a theroscilerosis, neurodegenerative diseases con treating or preventing metastatic cancer. Neurodegenerative diseases include for e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrapie. The agonists and attagonists of the polypeptide may be useful to treat osteoporosis, paged to give prion of bone implants particularly dental implants. Altered levels of human prostasin-like enzyme activity inhibit to both smooth muscle cell proliferation and lipid accumilation and inhibit to the progression of restenosis and atherosclerosis. Anti-human prostasin-like serime protease antibodies are useful for immunodetection and dispussions of micrometastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The present sequence represents the amino acid sequence of protein identified by Swiss Protein control of the progression of remparison studies with the human prostasin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.3%; Score 690; DB 5; 43.6%; Pred. No. 2.7e-46;
                                               Disclosure; Fig 3; 125pp; English
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Query Match

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176

g ò g à g à 셤 Homo sapiens

WO2003000012-A2.

Homo sapiens

ABJ37067

RESULT 11

Gaps

24;

Length 343;

us-10-037-417-46.rag

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or human polynucleotides or composition conquisation to the inversion and interpretation of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nagent that is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound useful in treating pain and animal of one or more of the polynucleotides given in the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that medulates its activity is useful for preparing a medicament for treating pain and spared nerve injury (CNI) in an animal segmental nerve injury (SNI) in an animal companies or this patent did not form part of the printed the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the value of the print of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                    Costigan M;
                                                                                                                                                                                                                                                                                                                                                                    Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page; 1017pp; English.
                                                                                                                                                                                                          01-NOV-2001; 2001US-03463B2P.
26-NOV-2001; 2001US-033347P.
                                                                                                                              14-AUG-2002; 2002WO-US025765.
                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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                        WO2003016475-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 TGWGHVAPSVSLLTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
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                                                                                                                                   1 MAQKGVLGPGQLGAVA---ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                      1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
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35.3%; Score 690; DB 7; Length 343;
43.6%; Pred. No. 2.7e-46;
ive 49; Mismatches 129; Indels 24; Gaps
Query Match
Best Local Similarity 43.61
Matches 156; Conservative
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or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector identifying a nucleotide, sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agente that increases or decreases the expression of the polymucleotide sequence with its differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially compound that regulates the activity of one or more of the composition, a method for identifying a compound or small molecule that regulates the activity of one or more of the regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound or small molecule that regulates the activity is useful for propagation or more of the polypeptides or their antibodies. The polymucleotide or the compound that mod a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. spinal teaching prepared presented is a human protein (shown in Table 2 of the rayersy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:
236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                          296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                     289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPWLSEH 343
                        The invention discloses a composition comprising two or more isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                              pain; neuronal tissue; gene therapy; segmental nerve injury; CCI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein Q16651, SEQ ID NO 13257.
                                                                                                                                                                                                                                                         ADD47561 standard; protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp; English.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woolf C, D'urso D,
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                                                                                                                                                                                                                                                                                                                                                                                                        RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; NOV14a; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis; arthritis; AIDsimmer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic;
Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic;
Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant;
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO ftp.wipo.int/pub/published pct_sequences.
                                                                                                                                                                                                                                      GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE
                                                                                                                                                                                                                                                                                                                                                            TGWGHVAPSVSLLTTPKPLQQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMYCAGYVEGG
                                                                                                                                                                                     MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPOARITGGSSAVA
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                                                                                                                         Gaps
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                                                                                          Length 343;
                                                                                         ; Score 690; DB 7; Length 34; Pred. No. 2.7e-46; 49; Mismatches 129; Indels
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10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-0274876P.
19-PAR-2001; 2001US-0284704P.
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                                                                                         Match 35.3%;
Local Similarity 43.6%;
les 156; Conservative 4
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                                                             Sequence 343 AA;
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Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA; Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM;

CURA-) CURAGEN CORP

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11;
                                                                                                                                                                                                                                               The present sequence is the protein sequence for a NOV protein. The NOV associated disorders are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, alleagies, blood disorders, ALDS, diabetes, obseity, astima, IgA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOV14a is a prostasin-like protein, and the NOV14a coding sequence localises to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115
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                                                                                                                                   or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLLRPILFLPLGLALG---LLSPWLSEH
ΜM;
Κ;
                                                                                                                               useful for prever
inflammation, or
tissue typing or
Tchernev VT, Miller CE, Guo X, Boldog FL, Grosse JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman I J, Malyankar U, Millet I, Peyman J, Smithson G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.0%; Score 645; DB 5; Length 30
'41.3%; Pred. No. 8.5e-43;
ive 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channel activating protease 1, (CAP1) protein.
                                                                                                                               NOVX polypeptides and encoding polynucleotides, treating NOVX-associated disorders e.g. cancer, Alzheimer's disease, and in chromosome mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                   Claim 1; Page 98; 358pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG72018 standard; protein; 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 41.3
Matches 148; Conservative
                                                Stone DJ;
                                                                                  2002-590674/63
                                                                                                                                                                                    pharmacodenomics.
                                                                                                   N-PSDB; ABN85392.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 307 AA;
 Taylor S, Tch
Alsobrook JP,
Macdougall J,
Gunther E, St
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PF Active-site 236..241

XX W0200283875-A2.

XX PW W0200283875-A2.

XX 24-OCT-2002.

XX E 29-MAR-2001; 2001US-0280509P.

PR 08-AUG-2001; 2001US-0210555P.

PR 29-MAR-2001; 2001US-0210555P.

RA 29-MAR-2002; 2002US-00109616.

XX A DELT-) DELTAGEN INC.

XX WEL 2003-058638/05.

DR WP1; 2003-058638/05.

DR WP1; 2003-058638/05.

DR WP2 20-MAR-2002; 2002US-00109616.

XX DR WP3 20-MAR-2003-058638/05.

DR WP3 29-MAR-2003-058638/05.

DR WP3 29-MAR-2003-058638/05.

DR WP3 29-MAR-2003-058638/05.

DR WP3 20-MAR-2003-058638/05.

DR WP3 20-MAR-2003-058638/05.

DR WP4 20-MAR-2003-058638/05.

DR WP5 2013-058638/05.

DR WP5 2013-0588/05.

DR WP5 201
```

Query Match
32.1%; Score 627.5; DB 6; Length 339;
Best Local Similarity 41.4%; Pred. No. 2.3e-41;
Matches 144; Conservative 48; Mismatches 139; Indels 17; Gaps 9;
Qy 1 MAQKGVLGPQQLGAVANSDSYSLYGLVPSG-PARG-PPYCGRP-EPSARIVGGSNAQPGT 57

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238 TCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRFGVFTAVATYEAWIREQVMGSEFGF 297
233 ACQGDSGGPLSCPMEGIWYLGAIVSMORGARPRFGYTLTSTYASWIIHTV - AELOP 290

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8

Search completed: February 25, 2004, 15:46:53 Job time : 104 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

February 25, 2004, 15:37:18; Search time 45 Seconds

(without alignments)
763.119 Million cell updates/sec

US-10-037-417-46 1953

Title: Perfect score:

1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	prostasin (EC 3.4.	Ω	tryptase (EC 3.4.2	mast cell proteina	enteropeptidase (E	tryptase (EC 3.4.2	EC 3.4	SG	tryptase (EC 3.4.2	allik	tryptase (EC 3.4.2	Ω	tryptage (EC 3.4.2	hepsin (EC 3.4.21.	plasma kallikrein	mast cell tryptase	acrosin (EC 3.4.21	acrosin (EC 3.4.21	plasma kallikrein	enteropeptidase (E	acrosin (EC 3.4.21	(BC	tryptase (EC 3.4.2	mastocytoma protei		(EC 3.4	(EC 3.4	(EC	(EC 3.4
SUMMARIES	ΙD	A57014	JC7731	A32410	A38654	A56318	JC4171	S00845	A35863	B35863	KQHUP	A45754	A53663	C35863	S33777	KOMSPL	856160	A37344	829599	KORTPL	A43090	JX0172	S47538	A47246	B32410	PLBO	A34170	S18407	A61545	B61545
	DB	н	N	Ŋ	N	~1	N	Н	N	7	Н	N	Н	7	н	н	7	N	7	н	⊢ 4	Ŋ	~	~	ผ	٦	Н	N	~	7
	Query Match Length	343	855	275	276	1019	274	417	275	275	638	274	1034	275	416	638	270	418	421	638	1035	436	431	273	269	812	415	437	455	460
do	Query	35.3	27.1	26.3	25.6	25.4	25.2	25.1	24.9	24.8	24.7	24.7	24.6	24.5	24.5	24.3	24.3	24.2	24.2	24.2	24.0	24.0	23.9	23.8	23.8	23.8	23.7	23.6	23.2	23.1
	Score	069	530	514.5	499	496	491.5	490.5	485.5	484.5	482.5	481.5	480	478.5	478.5	475	474.5	473.5	473	473	469.5	469	467.5	465.5	464.5	464.5	462		2	452
	Result No.		7	Э	4	<u>ب</u>	ø	7	00	σι	10	17	12	13	14	12	16	17	18	19	20	21	22	23	24	25	26	27	28	29

GQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLGAHQLDSYSE 110

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low-density lipopr	plasmin (EC 3.4.21	coagulation factor	plasmin (EC 3.4.21	plasmin (EC 3.4.21	plasmin (EC 3.4.21	coagulation factor	plasmin (EC 3.4.21	serine proteinease	polyprotein - Afri	pancreatic elastas	pancreatic elastas	tryptase (EC 3.4.2	testicular serine	acrosin (EC 3.4.21
JE0315	PLPG	KFHU1	B30848	PLHU	PLMS	KFHU12	I46260	A47547	T30337	A26823	B26823	S68702	JE0105	A55283
8 -	ıI	Н	7	Н	н	Н	~		7	N	7	7	7	7
1113	790	625	810	810	812	615	810	786	1524	269	269	237	366	420
23.1	22.9	22.9	22.8	22.7	22.6	22.5	22.3	22.3	22.2	22.1	22.1	22.0	22.0	21.8
452	448	447.5	445.5	442.5	440.5	440	436	435	434.5	432.5	431	429.5	429.5	426
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A;Note: parts of this sequence were determined by protein sequencing R;Yu, J.X.; Chao, L.; Chao, J.
J. Biol. Chem. 269, 18843-18848, 1994
A;Title: Prostasin is a novel human serine proteinase from seminal fluid. Purification, t A;Reference number: A54866; MUID:94308140; PMID:8034638
                                                                                                  C,Accession: A57014; A54866
R;Yu, J.X.; Chao, J.; Chao, J.
J. Biol. Chem. 270, 13483-13489; 1995
A;Title: Molecular cloning, tissue-specific expression, and cellular localization of hume A;Reference number: A57014; MUID:95286644; PMID:7768952
A;Accession: A57014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: GDB:676446; OMIM:600823
A,Cross-references: GDB:676446; OMIM:600823
A,Map position: 16p11.2-16p11.2
C,Superfamily: trypsin, trypsin, homology
C,Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein
F):33-44,45-343/Poroduct: prostasin #sratus predicted <MIT>
F):33-44,45-343/Pomain: prostasin light chain #status predicted <MIL>
F):45-343/Domain: prostasin heavy chain #status predicted <CHI>
F):45-341/Domain: trypsin homology <TRY>
F):32-341/Domain: trypsin homology <TRY>
F):32-314/Domain: trypsin homology <TRY>
F):32-315,70-86,168-244,201-223,234-262/Disulfide bonds: #status predicted
F):45-38/Active site: His, Asp, Ser #status predicted
F):59/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
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                               C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 21-Apr-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%; Score 690; DB 1; Length 343;
43.6%; Pred. No. 1.1e-46;
Live 49; Mismatches 129; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        \(\text{NICTOSS-references: GB:L41351; NID:9862304; PIDN:AAC41759.1; PID:9862305\)
prostasin (EC 3.4.21.-) precursor - human
                                                                                                                                                                                                                                                                                                                                      A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.3%;
Best Local Similarity 43.6%;
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein A; Residues: 45-64 < YUA>
                                                                                                                                                                                                                                                                                                                                                                                                                     A, Residues: 1-343 <RES>
                                                                                                                                                                                                                                                                                                                                                                              , Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: PRSS8
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A.Cross-references: GE:MS7626; NID:g200508; PIDN:AAA39988.1; PID:g200509
R;Reynolds, D.S.; Stevens, R.L.; Lane, W.S.; Carr, M.H.; Austen, K.F.; Serafin, W.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 3230-3234, 1990
A;Title: Different mouse mast cell populations express various combinations of at least A;Reference number: A35646; MUID:90222202; PMID:2326280
                                                                                                                                                                                                                                                                 Rivanderslice, P.; Craik, C.S.; Nadel, J.A.; Caughey, G.H.
Biochemistry 28, 4148-4155, 198
A;Title: Molecular cloning of 60g mast cell tryptase and a related protease: structural A;Reference number: A32410; MUID:89352460; PMID:2504277
A;Accession: A32410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M57625; NID:g200506; PIDN:AAA39987.1; PID:g200507
A;Note: the authors translated the codon CGC for residue 24 as Ala, GAG for residue 37
s Gly, GAG for residue 148 as Gly, GAG for residue 168 as Gly, and GAA for 185 as Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mast cell proteinase 6 (EC 3.4.21.-) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Accession: A38654; B38654; B35646; I59478
R;Reynolds, D.S.; Gurley, D.S.; Austen, K.F.; Serafin, W.E.
J. Balol. Chem. 266, 3847-3853, 1991
A;Title: Cloning of the cDNA and gene of mouse mast cell protease-6. Transcription }
A;Reference number: A38654; MUID:91139682; PMID:1995638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %;Cross-references: GB:MZ4664; NID:g163982; PIDN:AAA30854.1; PID:g163983; GB:J02862
C;Superfamily: trypsin; trypsin homology
C;Sewords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-30/Domain: activation peptide #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <ACT>
F;31-275/Product: tryptase #status predicted <AMT>
F;31-276/Domain: trypsin homology <TRY>
F;31-276/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELRLIGEATCQCLYSQPGPFNLTLQILPG-----MLCAGYPEGRRDTCQGDSGGPLVC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 KVPIVENSMCDVQY-----HLGLSTGDGVRIVREDMLCAG--NSKSDSCQGDSGGPLVC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
                                                                                                                                        tryptase (BC 3.4.21.59) precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LGSLVPVSPAP-----GQALQRVGIVGGREAPGSKWPWQVSLRLKGQYWRHICGGSLIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 SWVLSAAHCEMINGTLEPAAEWSVLL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GADLALIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPPWVLQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 LYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGG---GHICGGSLIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.3%; Score 514.5; DB 2; Best Local Similarity .42.2%; Pred. No. 4.8e-33; Matches 124; Conservative 27; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-276 <REY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-275 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A38654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Comment: This enzyme, an epithelial-derived, type II integral membrane serine protease of specific proteins or peptides on the brushborder membranes. It also participates in lial migration and/or cell loss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         membrane-bound arginine-specific serine proteinase precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 03-Feb-2003
C;Accession. 14.707731, 14.7731, 14.7731, 14.75430, 1.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda, R;Kishi, K.; Yamazaki, K.; Yasuda, I.; Yahagi, N.; Ichinose, M.; Tsuchiya, Y.; Athauda, J. Biochem. 130, 425-430, 2001
A;Rieler characterization of a membrane-bound arginine-specific serine protease from rat A;Reference number: JC7731; MUID:21421307; PMID:11530019
A;Accession: JC7731
A;Accession: JC7731
A;Accession: JC7731
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ILQKGEIRVINQTTCEELLPQ-----QITPRAMCVGFLSGGVDSCQGDSGGPLSS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 GGSLIAPSWVLSAAHCFMTNGTLEPA--AEWSVLLGVHSQD-GPLDGAHTRAVAAIVVPA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFNDFTFDYDIALLELEKPAEYSTVVRPICLPDNTHVFPAGKAIWVTGWGHTKEGGTGAL 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                      GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                             TGWGDVQBADPLPLPWVLQEVELRLLGBATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
                                                                                                                                                                                                                                                                                                                  236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYBAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 OPRVVPOTOESQPDSNLCGSHLAFSSAPAQGLIRPILFLFLELGLAG---LLSFWLSEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --ARIVGGSNAQPGTWPWQVSLHH-GGGHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 NYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: basolateral cell surface
C;Superfamily: membrane-bound arginine-specific serine proteinase
C;Keywords: protein digestion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.1%; Score 530; DB 2; Length 855; 39.9%; Pred. No. 1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CEEGGRWFQAGIISFGFGCGRRNRPGVFTAVATYBAWIREQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: DDBJ:AB037898
C;Comment: This arrest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.99
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: Small intestine
A; Accession: JC7775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: JC7775
A;Molecule type: mRNA
A;Residues: 1-855 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: mt-spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249
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*/prediction: cleaves activation peptide from trypsinogen to produce active trypsin A,Description: cleaves activation peptide from trypsinogen to produce active trypsin A,Desthary: intestinal digestive hydrolase cascade c'Superfamily: enteropedidase, Clr/Cls repeat homology; LDL receptor ligand-binding rept C,Superfamily: enteropedidase, Clr/Cls repeat homology; LDL receptor ligand-binding rept C,Reywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen F;1-284/Product: enteropedidase heavy chain #status predicted <HCA>
F;22-38/Domain: transmembrane #status predicted <HCA>
F;24-631/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;34-564/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;43-671/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;73-671/Domain: scavenger receptor ligand-binding repeat homology &LDL>
F;78-1019/Product: enteropedidase light chain #status predicted <LCH>
F;78-1019/Domain: trypsin homology <-RXP.
F;78-1019/Domain: trypsin homology <-RXP.
F;78-1014/1719,328 335,388,440,470,503,584,
F;71-286,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
F;772-866,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
F;78-5,971/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.; Maruyama, H.; Osada, Y.; Nē
                                                                                                                                         A,Map position: 21q21-21q21
C,Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tryptase (EC 3.4.21.59) precursor - rat
Nyllternate names: mast cell tryptase
Nyllternate names: mast cell tryptase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Aug-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000
C;Accession: JG4171
R;Ide, H.; Itch, H.; Tomita, M.; Murakumo, Y.; Kobayashi, T.; Maruyama, H.;
J. Biochem: 118, 210-215, 1395
A;Title: CDNA sequencing and expression of rat mast cell tryptase.
A;Accession: JG4171
A;Molecule type: mRNA
A;Residues: 1-274 <IDE>
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C;Comment: This enzyme is basically specific for a connective tissue mast ceinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||: ::||||||: |:||||| ::|| CGKKLAAQDITPKIVGSSNAKEGAWPWVGLYYGGRLLCGASLVSSDWLVSAAHC-VYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 TLEPAAEWSVLLGVHSQDGPLDGAHT--RAVAAIVVPANYSQVELGADLALLRLASPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      889 TDYIQPICLPEENQVFEPGRNCSIAGMGTVVYQGTTAN-----ILQEADVPLLSNERCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPAVWPVCLPRASHRFVHGTACWATGWGDV----QEADPLPLPWVLQEVELRLIGEATCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLYSQPGPFNLTLQ1LPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGR----PEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNG
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C;Keywords: glycoprotein; hydrolase; mast cell; serine proteinase; zymogen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-29/Domain: activation peptide #status predicted <ACT>
F;30-274/Product: mast cell tryptase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
or with amino-terminal myristoylation of the heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.4%; Score 496; DB 1; Length 101
39.2%; Pred. No. 5.6e-31;
Live 47; Mismatches 85; Indels
                                        C;Genetics:
A;Gene: GDB:PRSS7
A;Cross-references: GDB:384083; OMIM:226200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               996 ALPNRPGVYARVSRFTEWIO 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 GRRNRPGVFTAVATYEAWIR 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 102; Conservative
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Best Local
           otated below)
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A; Residues: 1-1019 < KITA-
A; Cross-references: GB:U09860; NID:g746412; PIDN:AACS0138.1; PID:g746413
R; Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. US.A. 91, 7588-7592, 1994
A; Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compc
A; Reference number: A43090; MUID:94329561; PMID:8052624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Residues: 749-1019 <KI2>
A.Cross-references: GB:U09860
C.Comment: The mechanism of association with the membrane of the intestinal brush border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enterokinase, the proteolyth
                                     A;Molecule type: protein
A;Residues: 32-54 <RE3>
R;Huang, R.; Abrink, M.; Gobl, A.E.; Nilsson, G.; Aveskogh, M.; Larsson, L.G.; Nilsson,
Scand. J. Immunol. 38, 359-367, 1993
A;Title: Expression of a mast cell tryptase in the human monocytic cell lines U-937 and
A;Reference number: I59478; MUID:94023807; PMID:8210998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYTGDDFPI-----VHDGMLCAG--NTRRDSCQGDSGGPLVCKVKGTWLQAGVVSWGEGC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEPAAEWSVILGVHSQDGPL-DGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SOPGPFNLTLQ1LPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEPSAR----IVGGSNAQPGTWPWQVSLHHGGG---HICGGSLIAPSWVLSAAHCFMTNGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-276 <RES>
A;Cross-references: GB:L31853; NID:g473480; PIDN:AAA39725.1; PID:g473481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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AjIntrons: 24/1; 79/2; 168/1; 222/3
CjSuperfamily: trypsin; trypsin homology
CjSuperfamily: trypsin; trypsin proteinase; zymogen
CjSuperfamils: signal sequence #status predicted <SIG>
F;22-31/Domain: activation peptide #status predicted <ACT>
F;22-31/Domain: mast cell proteinase 6 #status experimental <MAT>
F;32-268/Domain: trypsin homology <TRX>
F;75,122,225/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.6%; Score 499; DB 2; Length 276; 41.4%; Pred. No. 7.9e-32; Live 35; Mismatches 93; Indels ::
                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 41.48
Matches 109; Conservative
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A,Molecule type: protein
A,Residues: 31-38 <CRO>
A,Experimental source: pituitary
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A; Residues: 1-275 < VA2>
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Matches 11
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Biochemistry 27, 1067-1074, 1988
A; Title: A novel trypsin-like serine protease (hepsin) with a putative transmembrane dom A; References: S00845, MUID:88209431; PMID:2835076
A; Accession: S00845
A; Molecule type: mRNA
A; Residues: 1-417 < LEY>
A; Coss.references: EMBL:X07732; NID:932063; PIDN:CAA30558.1; PID:932064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 ASLGPAVWPVCLPRASHRFVHGTACWATGWGDV----QEADPLPLPWVLQEVELRLLGEA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 LPLTEYIQPVCLPAAGQALVDGKICTVTGWGNTQYYGQQAG-----VLQBARVPIISND 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 TCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEG----GRWFQAGI 260
                                                                                                                         9
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                                                                                                                                                                                                                                                152
                                                                                                                                                                                                                                                                                                                                 PAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY-- 210
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                                                                                                                                                                  47 IVGGSNAQPGTWPWQVSLHHGGG---HICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSV 103
                                                                                                                                                                                                         74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepsin (EC 3.4.21.-) - human
C,Species: Homo sapiens (man)
C,Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGRPE-PSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLE
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                                                                                                                                                                                                                                                                        GLYTGDDVPI-----VQDGMLCAG--NTRSDSCQGDSGGPLVCKVKGTWLQAGVVSWGEG
                                                                                                                                                                                                                                                ---AVAAIVVPANYSQVELGADLALLRLASPASLG
                                                                                                                                                                                                                                                                                                                                                                                                               ---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFG
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                                                                                                                           Gaps
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C. Genetics:
A, Genetics:
A, Genetics:
A, Cross-references: GDB:135685; OMIM:142440
A, Map position: 19911-19913.2
C, Superfamily: hepsin homology
C, Superfamily: hydrolase; liver; serine proteinase; transmembrane protein F;23-45/Domain: transmembrane #status predicted <TMN>
F;163-440/Domain: trypsin homology <TRY>
F;168-204,291-359,322-338,349-381/Disulfide bonds: #status predicted F;203,257,353/Active site: His, Asp, Ser #status predicted
                                                                                                                         43;
                     #status predicted (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 417;
                                                                         25.2%; Score 491.5; DB 2; Length 274; larity 40.2%; Pred. No. 3e-31; Conservative 20; Mismatches 07; Indels 43:
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                                                                                                                                                                                                         30 IVGGREASESKWPWQVSLRFKFSFWMHFCGGSLIHPQWVLTAAHC-
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F:30-266/Domain: trypsin homology <TRY>
F;73,120,223/Active site: His, Asp, Ser #status p:
F;131/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 CABANRPGIYTRVTYYLDWIHRYV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                     104 LLGVHSQDGPLDGAHTR
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Matches 111; Conserv
                                                                                  Query Match
Best Local Similarity
Matches 106; Conserv
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A; Accession, Accessio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VGPDVKDLAALRVQLREQHLYYQDQLL-----PVSRIIVHPQFYTAQIGADIALLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146 ASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGBAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 FMTNGTLEPAAEWSVLL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH-HG--GGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-275 <VAN>
A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M33491
R;Butterfield, J.H.; Weiler, D.A.; Hunt, L.W.; Wynn, S.R.; Roche, J. Leukoc. Biol. 47, 409-419, 1990
A;Title: Purification of tryptase from a human mast cell line.
A;Reference number: A60939; MUID:90244210; PMID:2110591
A;Accession: A60939
261 TSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQ 302
                                                                     C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase; zymogen
C;Keywords: hydrolase; serine proteinase; zerine
F;1-21/Domain: signal sequence #status predicted <ACI>F;22-30/Domain: activation peptide #status predicted <ACI>F;31-25/Product: tryptase I #status experimental <AMI>F;31-26/TDomain: tryptase I #status experimental <AMI>F;31-26/TDomain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser #status predicted
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A;Crosereferences: GDB:127575; OMIM:229000
A;Crosereferences: GDB:127575; OMIM:229000
A;Map position: 4d55-4d35
C;Superfamily: coagulation factor XI; trypsin homology
C;Serwords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflan C;Superfamily: signal sequence #status predicted <SIG>F;1-19/Domain: signal sequence #status predicted <SIG>F;20-109/Domain: apple repeat <AP2>F;20-109/Domain: apple repeat <AP2>F;10-199/Domain: apple repeat <AP2>F;20-109/Domain: apple repeat <AP2>F;20-109/Domain: apple repeat <AP2>F;20-109/Domain: apple repeat <AP2>F;20-108/Domain: apple repeat <AP2>F;20-108/Domain: apple repeat <AP2>F;20-108/Domain: apple repeat <AP3>F;20-108/Domain: apple repeat <AP3>F;20-108/Domain: plasma kallikrein light chain #status predicted <LCH>F;391-621/Domain: trypsin homology <TRY>F;31-634/Domain: trypsin homology <TRY>F;31-104,47-77;51-55,231-237,292-375,322-328,383-F;21-104,47-37,513-45/Disulfide bonds: #status predicted (coagulation factor XIIa) #status predicted F;316-347,340-345/Disulfide bonds: #status predicted (coagulation factor XIIa) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Molecule type: protein
A; Residues: 20-27; 40-46, X', 48, 'H', 50, 'X', 52-70, 'H'; 75-76, 'X', 78-80; 103-113; 131-140; 141-7; 126-283, 'X', 285; 287-231, 'X', 293-295; 314-317, 'X', 319-320; 321-324; 'X', 329-333; 334-339, 'X', 525; 538-51562, 'X', 564-567; 573, 'X', 575-56; 578-583, 'X', 585; 592-604 A(MC)
C; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex winc; C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a lighar linked by one or more disulfide bonds.
C; Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal reinnogen and may also play a role in the renin-angiotensin system by converting prorenin in C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: mRNA
A;Residues: 1-638 cCHU>
A;CROSI-TECERCECS: GRN3143; NID:g190262; PIDN:AAA60153.1; PID:g190263
A;CROSI-TECERCECS: GRN3143; NID:g190262; PIDN:AAA60153.1; PID:g190263
R;McMillen, B.A.; Fujikawa, K.; Davie, E.W.
Biochemistry 30, 2050-2056, 1991
Biochemistry 30, 2050-2056, 1991
A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of
A;Reference number: A37939; MUID:91152016; PMID:1998666
                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 18-Jun-1999
C;Accession. A00921; A37939
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
A;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.
A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four A;Reference number: A00921; MuID:86243359; PMID:3521732
A;Accession: A00921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 KPICLPSKGDTSTIYTNCWVTGWGFSKEKGEIQN--ILQKVNIPLVTNEECQKRYQD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 SARIVGGSNAQPGTWPWQVSLH---HGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388 STRIVGGTNSSWGEWPWQVSLQVKLTAQRHLCGGSLIGHQWVLTAAHCF---DGLPLQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 WSVLLGV-----HSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAV
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40.2%; Pred. No. 3.9e-30;
tive 33; Mismatches 97;
                                                                                                                                                      N;Alternate names: kininogenin; plasma prekallikrein
                                                                                                                  (EC 3.4.21.34) precursor - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104; Conservative
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                                                                                                                  plasma kallikrein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: KLK3
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A; Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine pr
A; Reference number: A35863; MUID:90251647; PMID:2187193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA; DNA
A; Residues: 1-275 <VAN.
A; Cross-references: GB:M33492; NID:G339982; PIDN:AAA36779.1; PID:G339983
A; Cross-references: GB:M3492; NID:G339982; PIDN:AAA36779.1; PID:G339983
A; Note: residues 2-275 are derived from mRNA; residue one was inferred from the genomic R; Miller, J.S.; Moxley, G.; Schwartz, L.B.
Clin. Invest. 86, 864-870, 1990
A; Title: Cloning and characterization of a second complementary DNA for human tryptase.
A; Reference number: A37193; MUID:90369005; PMID:2203827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: mRNA
A, Residues: 1-275 < MIL>
A, Residues: 1-275 < MIL>
A, Cross-references: GB: M37488; NID: g179583; PIDN: AAA51843.1; PID: g179584
R, Ellom, T.; Hellman, L.
Scand, J. Immunol. 37, 203-208, 1993
A, Title: Characterization of a tryptase mRNA expressed in the human basophil cell line
A, Reference number: I59473; MULD: 93166209; PMID: 8434231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 FMTNGTLEPAAEWSVLL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRL 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 EEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHI 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 ASPASLGPAVWPYCLPRASHRFVHGTACWATGWGDYQEADPLPLPWVLQEYELRLIGEAT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 COCLYSQPGPFNLTLQIL-PGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75
                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 21-Jul-2000
C;Accession: B35863; A37193; Ī59473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYAAPAPGQALQRVGIVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH-HG--GGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-275 <RES>
A;Cross-references: GB:S5551; NID:g265666; PIDN:AAD13876.1; PID:g4261576
A;Experimental source: basophil cell line KU812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.8%; Score 484.5; DB 2; Length 275; 41.7%; Pred. No. 1.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Kewwords: hydrolase; serine proteinase; zymogen
;1-21/Domain: signal sequence #starus predicted <SIG>
;22-30/Domain: activation peptide #starus predicted <ACT>
;31-275/Product: tryptase I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,74,121,224/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 FGCGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 EGCAOPNRPGIYTRVTYYLDWIHHYV 271
                                                                                                                                                                                                               tryptase (EC 3.4.21.59) II precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:125890; OMIM:191080
EGCAQPNRPGIYTRVTYYLDWIHHYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: trypsin; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-267/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                           N;Alternate names: tryptase beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 41.7
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Map position: 16pter-16gter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: I59473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A37193
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8 g à q à д

RESULT 11

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A; Packing activation peptide from trypsinogen to produce active trypsin A; Pathway: intestinal digestive hydrolase cascade
A; Pathway: intestinal digestive hydrolase cascade
C; Superfamily: enteropeptidase; CIr/CIs repeat homology; LDL receptor ligand-binding rep
C; Superfamily: enteropeptidase; serine proteinase; transmembrane protein; zymogen
C; Scywords: alycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
F; 22-38/Domain: transmembrane #status predicted <ff>F; 22-117/Product: enteropeptidase mini chain #status predicted <ff>HCH>
F; 118-799/Product: enteropeptidase heavy chain #status predicted <ff>HCH>
F; 118-799/Promain: LDL receptor ligand-binding repeat homology <LDLL>
F; 535-519/Domain: CIr/CIs repeat homology <ff>F; 541-646/Domain: CIr/CIs repeat homology <ff>F; 541-646/Domain: LDL receptor ligand-binding repeat homology & LDLL>
F; 693-798/Domain: LTrypsin homology <ff>F; 693-798/Domain: LTrypsin His, ASP, 695-518, 549, 645, 697, 701, 721, 740, 761, 804, 863, 902, 96</f>
F; 787-911, 825-841, 925-992, 956-971, 982-1010/Disulfide bonds: #status predicted
F; 840, 891, 986/Active site: His, ASP, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M33494; NID:g3927804; PIDN:AAC83172.1; PID:g339977
A;Note: the first nine regidues of this sequence are inferred from genomic DNA of trypts
A;Cross-references: GB:D30799; NID:g505122; PIDN:BAA06459.1; PID:g505123
A;Note: parts of this sequence, including the amino ends of three chains isolated from t C;Comment: The mechanism of association with the membrane of the intestinal brush border otated below) or with amino-terminal myristoylation of the heavy chain.
C;Complex: Mature enteropeptidase is variously reported to contain two (heavy and light) ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 07-Mar-2003
C;Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text_change 07-Mar-2003
C;Accession: C35863; E35863; A38893
E;Vanderslice, P.; Ballinger, S.M.; Tam, E.K.; Goldstein, S.M.; Craik, C.S.; Caughey, Proc. Natl. Acad. Sci. U.S.A. 87, 3811-3815, 1990
A;Title: Human mast cell tryptase: multiple cDNAs and genes reveal a multigene serine A;Reference number: A35863; MUID:90251647; PMID:2187193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 CGR----PEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 TLEPAAEWSVLLGVHSQDGPLDGAH--TRAVAAIVVPANYSQVELGADLALLRLASPASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 GPAVWPVCLPRASHRFVHGTACWATGWGDV-OEADPLPLPWVLQEVELRLLGEATCQCLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGIISFGFGCGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.6%; Score 480; DB 1; Length 10
38.5%; Pred. No. 1e-29;
tive 46; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tryptase (EC 3.4.21.59) III precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1014 NRPGVYARVPKFTEWIQ 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to GenBank, April 1990
A;Reference number: A38893
A;Accession: A38893
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Best Local Similarity 38.5%
Matches 99; Conservative
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A, Molecule type: mRNA
A, Residues: 9-275 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: E35863
A;Molecule type: DNA
A;Residues: 1-9 <VA2>
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C35863
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A,Molecule type: mRNA
A,Residues: 1-274 <MIZ.>
A,Residues: 1-274 <MIZ.>
A,Residues: 1-274 <MIZ.>
A,Cross-references: GB:M3003B
A,Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 205-Pro
C,Superfamily: trypsin; trypsin; homology, zymogen
C,Superfamily: trypsin; trypsin bomology, zymogen
F,1-21/Domain: activation peptide #status predicted <SIG>F;22-30/Domain: activation peptide #status predicted <ACT>
F,31-266/Domain: trypsin homology <TRX>
F,31-266/Domain: trypsin homology <TRX>
F,74,120,223/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enteropeptidase (EC 3.4.21.9) precursor [validated] - pig
NyAlternate names: enterokinase
C;Species: Sus serofa domestica (domestic pig)
C;Species: Sus serofa domestica (domestic pig)
C;Accession: A5363
E;Accession: A5363
My atsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, J. Biol. Chem. 269, 19976-19982, 1994
A;Pitle: Structural characterization of porcine enteropeptidase.
A;Reference number: A53663, WUID:94327548; PMID:8051081
A;Accession: A5363
A;Molecule type: mRNA
A;Residues: 1-1034 <AMIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA

A; Residues: 1-274 < MILD.

A; Residues: 1-274 < MILD.

A; Cross-references: GB: MA30038

R; Miller, J.S.; Moxley, G.; Schwartz, L.B.

A; Clin. Invest. 86, 864-870, 1990

A; Title: Cloning and characterization of a second complementary DNA for human tryptase.

A; Reference number: A37193; MUID:90369005; PMID:2203827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 --LGPDVKDLATLRVNS-----GTHLYYQDQLLPVSRIMVHPQFYIIQTGADIALLELE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 SPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVBLRLLGBATC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                        C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 08-Sep-1997 C;Accession: A45754; B37193 R;Miller, J.S.; Westin, E.H.; Schwartz, L.B. C;Lin, Invest. 84, 1188-1195, 1989 A;Title: Cloning and characterization of complementary DNA for human tryptase. A;Reference number: A45754; MUID:90009311; PMID:2677049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 QCLYSQPGPFNLTLQIL-PGMLCAGYPBGRRDTCQGDSGGPLVCBEGGRWFQAGITSFGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 PADVQALQQAGIVGGQBAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 PEP----SARIVGGSNAQPGTWPWQVSLH---HGGGHICGGSLIAPSWVLSAAHCFMTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 24.7%; Score 481.5; DB 2; al Similarity 40.8%; Pred. No. 1.8e-30; 108; Conservative 31; Mismatches 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAOPNRPGIYTRVTYYLDWIHHYV 270
                                                                                                                                                                                                                  tryptase (EC 3.4.21.59) alpha precursor
C;Species: Homo sapiens (man)
                                  611 YTKVAEYMDWILEKTQSSD
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Query Match Best Loca Matches

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Biochim. Biophys. Acta 1173, 350-352, 1993
A;Title: Cloning and sequence analysis of rat hepsin, a cell surface serine proteinase.
A;Reference number: S33777; MUID:93305733; PMID:8318546
A;Accession: S33777
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQEVELRLLGBATCQCLY 210
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                                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 18-Jun-1999
C;Accession: S33777; S32013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||| : | ||||| :: | ||||||| : | ||||||| | CGRRKLPVDRIVGGODSSLGRWFFAHCGGSLLSGDWVLTAAHCFPERNRV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 PAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQV-----ELGADLALLRLASPAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEPVNVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPPPLKQVKVPIMENHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQCLYSQPGPFNLTLQIL-PGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFG
                                                                                                                                                                                                                                                                                                                        32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLH---HGGGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                     AYAAPAPGQALQRVGIVGGQBAPRSKWPWQVSLRVRDRYWMHFCGGSLIHPQWVLTAAHC
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A, Residues: 9-131, 'K', 132-275 < VA3>
A, Cross-references: GB:M33493; NID:g339984; PIDN:AAA36780.1; PID:g339985
C, Superfamily: trypsin, trypsin, homology
C, Superfamily: trypsin; trypsin, trypsin, trypsin, trypsin, trypsin homology
C, Keywords: hydrolase; serine proteinase; zymogen
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-30/Domain: activation peptide #status predicted <ACT>F;2-30/Domain: trypsin homology <TRY>F;31-267/Domain: trypsin homology <TRY>F;31-267/Domain: trypsin homology <TRY>F;74,121,224/Active site: His, Asp, Ser #status predicted
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                                                                                                                                                                                                                             24.5%; Score 478.5; DB 2; Length 41.0%; Pred. No. 3.2e-30; Live 32; Mismatches 108; Indels
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Matches 109; Conservative
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Matches 107; Conserv
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A, MoLeoule Cype: maked A, Moleoule Cype: maked A, Residues: 1-638 cSEL>
A, Cross-references: GB:M58588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A, Cross-references: GB:M58588; NID:g200358; PIDN:AAA63393.1; PID:g200359
A, Note: part of this sequence, including the amino ends of both the heavy and light chair C; Comment: This protein, synthesized in the liver, circulates as a noncovalent complex wi C; Comment: The zymogen is activated by factor XIIa, which cleaves the molecule into a light are linked by one or more disulfide bonds.
C; Superfamily: coagulation factor XI; trypsin howlogy
C; Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; inflam C; Zy20-109/Domain: signal sequence #status predicted <SIG>E; 20-309/Product; plasma kallikrein heavy chain #status experimental <HCH>E; 20-109/Domain: apple repeat <AP2>E; 20-109/Domain: apple repeat <AP2>E; 20-109/Domain: apple repeat <AP2>E; 20-109/Domain: apple repeat <AP4>E; 391-638/Product: plasma kallikrein light chain #status experimental <LCH>E; 21-104, 47-7, 51-57, 111-194, 137-166, 141-147, 201-284, 227-256, 231-237, 292-375, 318-347, 332-571, 217, 215, 308, 396, 494/Rainding site: carbohydrate (ABN) (covalent) #status predicted E; 434, 483, 578/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                 plasma kallikrein (EC 3.4.21.34) precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1992 #text_change 18-Jun-1999 C;Accession: 30-Sep-1992 #text_change 18-Jun-1999 C;Accession: A35557 C;Accession: A35557 As 1990 A; Hamelin, J.; Mion, P.; Beaubien, G.; Brachpapa, L.; Rochemont DNA cll Biol. 9, 737-748, 1990 A;Attle: Mouse plasma kallikrein: cDNA structure, enzyme characterization, and comparison A;Reference number: A36557; MUID:91090844; PMID:2264928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 QVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEBG 252
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211 SOPGPFNLTLOILPGMLCAGYPEGRRDTCQGDSGGPLVCEE----GGRWFQAGITSFGFG 266
                                                           73 GGSLIAPSWVLSAAHCFWINGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 SSGYSLRLCKLVDS-----PDC-TTKINARIVGGTNASLGEWPWQVSLQVKLVSQTHLC
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 25, 2004, 14:37:37; Search time 49 Seconds (without alignments) 379.368 Million cell updates/sec Run on:

US-10-037-417-46 1953 1 MAQKGVLGFCQLGAVANSDSTKSLVLPWLSPHSLLGLWGF 357 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

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Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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322
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its work by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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                                   kidney, lung, pancreas, colon, bronchus and renal proximal tubular cells. In the prostate gland it may be synthesized in epithelial cells, secreted into the ducts, and excreted into the seminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Gaps
     SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS.
                           TISSUE SPECIFICITY: Found in prostate, liver, salivary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -LINKED (GLCNAC. . .) (POTENTIAL) 98DD6447F5A8C1B2 CRC64;
                                                                                                                                                                                                                                                                      A GO, GO:0005615; C:extracellular space; TAS.

GO; GO:0005826; C:plasma membrane; TAS.

GO; GO:0008236; F:serine-type peptidase activity; TAS.

IncerPro; IPR001254; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1.

InterPro; IPR001314; Peptidase_S1A.

Refin; PF00089; LTYPSiI, 1.

R PRINTS; PR00722; CHYMCTRYBSIN.

R RMART; SM0020; TYP_SEN; I.

R PROSITE; PS00134; TRYPSIN DOM; I.

R PROSITE; PS00135; TRYPSIN DOM; I.

R HYGGITE; PS00135; TRYPSIN HIS; I.

Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein; Iransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 343;
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BY SIMILARITY.
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
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ACTIVATION PEPTIDE.
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.3%; Score 690; DB 1; 43.6%; Pred. No. 1.1e-47;
                                                                              SIMILARITY: Belongs to peptidase family S1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SERINE PROTEASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36431 MW;
                                                                                                                                                                                                           EMBL; BC001462; AAH01462.1; -.
                                                                                                                                                                                      EMBL; L41351; AAC41759.1; -. EMBL; U33446; AAB19071.1; -.
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                                                                                                                                                                                                                                HSSP; P00763; 1DPO.
MEROPS; S01.159; -.
Genew; HGNC:9491; PRSSB.
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223
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disulfide bond.
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PROPEP
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                                                                                                                                                                    TGWGDVQBADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGR 235
                                                           171 TGWGHVAPSVSLLTPKPLÖQLEVPLISRETCNCLYNIDAKPEEPHFVQEDMVCAGYVEGG 230
                                                                                                                                 236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                               296 GPAFPTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLVLPWLSPH 349
                                                                                                                                                                                                                                                                                                   289 QPRVVPQTQESQPDSNLCGSHLAFSSAPAQGLIRPILFLPLGLALG---LLSFWLSEH 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIANE=20235202; PubMed=10770960; Vagatar C., Bens M., Farman N., Vaagniaux G., Vallet V., Jaeger N.F., Pfister C., Bens M., Farman N., Courtois-Coutry N., Vandewalle A., Rossier B.C., Hummler E., Activation of the amiloride-sensitive epithelial sodium channel by the serine protease mCAP1 expressed in a mouse cortical collecting duct cell line.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Prostasin precursor (EC 3.4.21.-) (Channel activating protease 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
ACTIVATION PEPTIDE (BY SIMILARITY).
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342 AA
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InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Fram; PF001039; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM0020; Tryp_SPC; 1.
PROSITE; PS00130; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
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HSSP; P00734; 1UVS.
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113 VVHTVAQIITHSSYREEGSQGDIAFIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTG 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 WPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE---AYEVKLGAHQLDSYSNDT 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG
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SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Possesses a trypsin-like cleavage specificity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                                                                                                              32.3%; Score 631; DB 1; Length 342; 41.4%; Pred. No. 5.2e-43; ive 48; Mismatches 139; Indels
BY SIMILARITY.
POTENTIAL.
SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SYSTEM CHARGE RELAY SYSTEM (BY SYSTEM SYSTEM C
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Adachi M., Kitamura K., Miyoshi T., Tomita K.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
26-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                 36729 MW;
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342 AA;
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                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 WPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGA
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// SIMILARITY).
// SIMILARITY).
// POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 342;
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BY SIMILARITY.
BY SIMILARITY.
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CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL CHARGE RELAY SYSTEM (BY SIMIL
                                                                                                                                                                                                                                                                                       Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.7%; Score 620; DB 1; Length 34 40.8%; Pred. No. 3.9e-42; ive 50; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5ED1AF05D9213B98 CRC64;
                                                                                                                                                                                                                                                                                                                            ACTIVATION PEPTIDE (BY PROSTATIN LIGHT CHAIN.
                                                                                                                                                                                                                                                                                                                                            PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
BY SIMILARITY.
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I -> V (IN REF. 1).
A -> V (IN REF. 1).
SIMILARITY: Belongs to peptidase family S1
                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE.
                                                                                                                                                     HSSP; P00734; 1UVS.
InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_51.
InterPro; IPR001314; Peptidase_51.
InterPro; IPR001314; Peptidase_51A.
Pfan; Pr00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM0020; Tryp_SPC; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                             EMBL; AB017638; BAB20281.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36843 MW;
                                                                                                                                           EMBL; AF202076; AAG32641.1;
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1068
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321 AA;
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                                          DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mittman S., Agnew W.S.;
"Organization and alternative splicing of CACNAIH.";
"Organization and alternative splicing of CACNAIH.";
"Organization and alternative BMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane-anchored (Potential).
-!- TISSUB SPECIFICITY: Expressed in many tissues.
-!- POLYMORPHISM: There are two alleles; gamma-I and gamma-II which differ by 5 residues.
-!- SIMILARITY: Belongs to peptidase family SI. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=99452974; PubMed=10521469;
Wong G.W., Tang Y., Feyfant B., Sali A., Li L., Li Y., Huang C.,
Wong G.W., Tang X., Stevens R.L.;
Friend D.S., Krilis S.A., Stevens R.L.;
"Identification of a new member of the tryptase family of mouse and
human mast cell proteases which possesses a novel COOM-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of human gamma-tryptases, novel members of the chromosome 16p mast cell tryptase and prostasin gene families."; J. Immunol. 164:6566-6575(2000).
                                                                                                                                                                                                                                                                                                                                MEDLINE=20302813; PubMed=10843716;
Caughey G.H., Raymond W.W., Blount J.L., Hau L.W., Pallaoro M.,
Wolters P.J., Verghese G.M.;
                                                                                                                                                         (Transmembrane tryptase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IRR000003; Cys.Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1.
Pfam; Pr00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSTIE; PS00134; TRYPSIN DOM; 1.
PROSTIE; PS00134; TRYPSIN HIS; 1.
PROSTIE; PS00135; TRYPSIN SER; FALSE NEG.
Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
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TRYPTASE GAMMA HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (VARIANTS GAMMA-1 AND GAMMA-2)
                      TRYG HUMAN STANDARD; PRT; 321 AA. QONERZ; Q9CO15; Q9NRQB; Q9UBB2; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last sequence update) Tryptase gamma precursor (RC 3.4.21.-) (Transmitted on Thm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hydrophobic extension.";
J. Biol. Chem. 274:30784-30793(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF191031; AAF76457.1; --
EMBL; AF195508; AAF76458.1; --
EMBL; AF175759; AAF03697.1; --
EMBL; AF17552; AAF03695.1; --
EMBL; AF223663; AAF48852.2; --
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 220-321 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ransmembrane; Polymorphism.
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                                                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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           RESULT 4
TRYG_HUMAN
                                                                        THEFFER AND BREEFFER BREEFFER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148
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                                                                                                                                                                                                                                                                                                                                                                                                                       24 PGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRIRRMHVCGGSLLSPQWVLTAAHCF--S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 GILEPAAEWSVLLGVHSQDGPLD---GAHTRAVAAIVVPANYS-QVELGADLALLRLASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 ASLGPAVWPYCLPPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 LYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2003 (Rel. 42, Last annotation update)
Pancreasin precursor (EC 3.4.21.-) (Marapsin) (Channel-activating protease 2) (CAPH2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-22439795; PubMed-12441343;
Bhagwandin V.J., Hau L.W.-T., Mallen-St Clair J., Wolters P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             serine
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                 29.8%; Score 582; DB 1; Length 321; 46.0%; Pred. No. 3.7e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fortunato M., Dando P.M., Rawlings N.D., Barrett A.J.; "Cloning, sequencing and expression of marapsin, a human
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Okaze H., Hayashi A., Kozuma S., Saito T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
            269 KRNRPGVFTAVATYEAWIREQVM---GSEPGPAFPTQP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 RPNRPGVYTRVPAYVNWIRRHITASGGSESG--YPRLP 283
                                                                                                                                                                                                                                                                                                                                                                  87;
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                                                                                                                                                                                                                                                                                                       33827 MW;
                                                                                                                                                                                                                                                                                                                                                      46.08;
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.0%
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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T 6
HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 NGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPAN--YSQVELGADLALLRLASPA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AKAATACGRPRMINRMVGGQDTQEGEWPWQVSIQRNGSHFCGGSLIAEQWVLTAAHCF-- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
        "Structure and activity of human pancreasin, a novel tryptic serine
                                                                                                                                                                                                                                                                                                                                                                                        SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%; Score 563; DB 1; Length 290;
ilarity 42.2%; Pred. No. 1.1e-37;
Conservative 32; Mismatches 114; Indels 14;
                 peptidase expressed primarily by the pancreas.";
J. Biol. Chem. 278:3363-3371(2003).
-i. SUBCELBUIAR LOCATION: Secreted.
-i. TISSUE SCIFICITY: Expressed predominantly in the pancreas.
-i. FTM: N-91ycosylated.
-i. SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein.
SIGNAL
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Fram; PF00009; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SWART; SM00020; Tryp_SPC; 1.
PROSITE; PS00130; TRYPSIN LOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PANCREASIN
                                                                                                                                                                            EMBL, AJ306593; CAC35467.1; -. EMBL; AB056161; BAB85497.1; -. EMBL; AY030095; AAK38168.1; -. HSSP; P00734; 1UVS. MEROPS; S01.074; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31940 MW;
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hes 117; Conserv
Caughey G.H.;
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DOMAIN
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ACT SITE
ACT SITE
DISULFID
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Matches
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Replacement II. Schweigh R. F., Texter P. A., Rubin G. M. Bong I. S. Bendelendo L., Warnein R. M. F., Casavant T. L., Scheetz T. E., Raplacement M. S., Unddin T. B., Tonhyldis S., Carring P. N. Range G. J., Range G. J., Alxamson R. D., Mullady S. J., Range G. J., Alxamson R. D., Mullady S. J., Loquelland N. A., Peters G. J., Alxamson R. D., Mullady S. J., Alxamson R. D., Mullady S. J., Range G. J., Mark J. A., Gomarton P. H., Richard S. J., Mark J. A., Gomarton P. H., Richard S. J., Mark J. A., Gomarton P. H., Richard S. J., Mark J. A., Gomarton P. H., Richard S. J., Mark J. A., Gomarton P. H., Richard S. J., Mark J. A., Gomarton P. J., Richard S. J., Mark J. A., Gomarton P. J., Richard S. J., Mark J. A., Gomarton P. J., Richard S. J., Mark J. A., Gomarton D. M., Mark J. A., Gomarton D. M., Mark J. A., Gomarton D. J., Mark J. A., Schell J. J. J., Gomer S. J. M., Schell J. J. J., Johnson J. J., Mark J. M., Schell J. J. J., Johnson J. J., Mark J. M., Schell J. J. J., Johnson J. J., Mark J. M., Schell J. J. J., Johnson J. J., Mark J. Mark J. J. Mark J. J. J., Gomer S. J. M., Schell J. J. J., Johnson J. J., Mark J. J., Mark J. J. J., Schell J. J. J., Johnson J. J. J. J., Johnson J. J. J., Johnson J. J. J., Johnson J. J. J., Johnson J. J., Jo
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218 LILOILPGMICAGYPEGRRDTCQGDSGGPLVCEE-GGRWFQAGITSFGFGCGRRNRPGVF 276
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PROSITE; PS01180; CUB; 1.
PROSITE; PS01209; LDLRA_1; 1.
PROSITE; PS50068; LDLRA_2; 3.
PROSITE; PS500240; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_ER; 1.
Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane; Glycoprotein; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
55 CYTOPLASMIC (POTENTIAL).
66 76 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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09GZN4; 043342;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
18-ABAIN-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4)
PRSS22 OR PRSS26 OR BSSP4.
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/FTIG=VSP 008380.
A -> V (IN REF. 4).
7EEF193F655DDE9D CRC64;
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LLL-RECEPTOR CLASS A 2.
LLL-RECEPTOR CLASS A 3.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY STRARGE RELAY SYSTEM (BY GHARGE RELAY
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A MEDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jedeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,

B Apatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Apatchenko L., Marusina M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Raha S.B., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzzy D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Raha J., Helton E., Setteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rabakesley R.W., Touchman J.W., Gremen B.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

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                                   Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               Mitsui S., Okui A., Kominami K., Yamaguchi N.; "Cloning and characterization of a human brain-specific serine protease, hBSSP-4.";
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
PERM; PP00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
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Genew; HGNC:14368; PRSS22.
sapiens (Human)
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67 GGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIV 126
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"Molecular cloning of cDNA for matriptase, a matrix-degrading serine
protease with trypsin-like activity.",
J. Biol. Chem. 274:18231-18236(1999).
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"Reverse biochemistry: Use of macromolecular protease inhibitors to dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                                                                                                                                   CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
L -> M (IN REF. 4).
M, EZALZ3BC86E79935 CRC64;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
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                                                                                                                                                           BRAIN-SPECIFIC SERINE PROTEASE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.9%; Score 544; DB 1; 39.3%; Pred. No. 3.8e-36;
                                                                             Hydrolase; Serine protease; Signal.
SIGNAL 1 32 POTENTIAL
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MEDLINE=99303581; PubMed=10373424;
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TRYPSIN HIS; 1.
TRYPSIN SER; 1.
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33731 MW;
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Best Local Similarity
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                                                                                                                                                                                                                                   TISSUENCE FROM N.A.

TISSUENCE FROM N.A.

TISSUESION and Muscle;

TISSUESION TO THE MATCLE;

MEDLINE=2238827; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MAISCHUI S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MAISCHOP L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Fonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Fonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ugdin T.B., Forbiyaki S., Carninci P., Prange C.,

Raha S.A., McEwan P.J., McKernan K.J., Malak J.A., Gluba R.A.,

Richards S.A., McEwan P.J., McKernan K.J., Malak J.A., Gluba R.A.,

Richards S.A., McEwan P.J., McKernan K.J., Madan A., Godrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Raha S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Milk;

MEDITALE-99303622, PubMed=10373425;

MEDITALC.W., Anders J., Johnson M., Dickson R.B.;

"Purification and characterization of a complex containing matriptase and a Kunitz-type serine protease inhibitor from human milk.";

J. Biol. Chem. 274:18237-18242(1999).

J. FUNCTION: Degrades extracellular matrix. Proposed to play a role
                       Yamaguchi N., Mitsui S.;
mMolecular cloning of a novel transmembrane serine protease expressed
in human prostate ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanimoto H., Underwood L.J., Wang Y., Shigemasa K., Parmley T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 340-664 FROM N.A.
Cao J., Fan W., Zheng S.;
"Genomic analysis of a novel human serine protease SNC19.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                 Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                         O'Brien T.J.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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EMBL; AF130086; AAF00109.1; --
EMBL; AB030036; BAB20376.1; --
EMBL; AF057145; AAG15395.1; --
EMBL; BC005826; AAH30526.1; --
EMBL; BC305825; AAH30532.1; --
EMBL; AF283256; AAG13949.1; --
HSSP; P00763; 1DPO.
Genew; HGNC:11344; ST14.
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SEQUENCE FROM N.A.
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                                                              human prostate
IISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 CGGSLIAPSWVLSAAHCFMTNG--TLEPAAEWSVLLGVHSQ-DGPLDGAHTRAVAAIVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 LPWVLQEVELRLIGERATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

FER -> GTR (IN REF. 5; ARHOS826).
R MIM, 606797; -..

R MRROPS; SOI.1302; -..

R GO; GO:0008286; F:serine-type peptidase activity, TAS.

GO; GO:0008286; F:serine-type peptidase activity, TAS.

GO; GO:0006508; P:proteolysis and peptidolysis; TAS.

R InterPro; IPR000899; CUB.

R InterPro; IPR001254; Peptidase_SI.

InterPro; IPR001254; Peptidase_SI.

R InterPro; IPR001254; Peptidase_SI.

R InterPro; IPR001214; Peptidase_SI.

R Pfam; PF000431; CUB; 2.

R Pfam; PF000431; CUB; 2.

R Pfam; PF000431; CUB; 2.

R RRINTS; PR00125; LDLRECEPTOR.

R SMART; SM00042; CUB; 2.

R SMART; SM00020; TYPESPE; 1.

R PROSITE; PS01209; LDLRA 1; 2.

R PROSITE; PS0139; TRYPSIN DOM; 1.

R PROSITE; PS0139; TRYPSIN DOM; 1.

R PROSITE; PS0139; TRYPSIN JES; 1.

R PROSITE; PS0139; TRYPSIN MIS; 1.

R PROSITE; PS0139; TRYPSIN MIS; 1.

R PROSITE; PS0139; TRYPSIN MIS; 1.

R PROSITE; PS0139; TRYPSIN SER; 1.

R PROSITE; PS01409; LDLRA 2; 2.

R PROSITE; PS01409; LDLRA 2; 3.

R PROSITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
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Isold=Q9Y6M0-2; Sequence=VSP_005389;
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 Inoue M., Kanbe N., Kurosawa M., Kido H., ^{\prime} Cloning and tissue distribution of a novel serine protease esp-1 from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hooper J.D., Bowen N., Marshall H., Cullen L.M., Sood R., Daniels R., Stuttgen M.A., Normyle J.F., Higgs D.R., Kastner D.L., Ogbourne S.M., Pera M.F., Jaxwinska E.C., Antalis T.M., "Localization, expression and genomic structure of the gene encoding the human serine procease testisin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22881296; PubMed=12975309;
MEDLINE=22881296; PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chan J., Chow B., Cruit C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Godowski P.;
                                                  Q9Y6MO; Q9NS34; Q9P2V6; 16-007-2001 [Rel. 40, Created) 16-007-2001 [Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) 15-MAR-2004 (Rel. 43, Last annotation update) 17-615.5 more cursor (BC 3.4.21.-) (Bosinophil serine protease 1) (BSP-PRSS21 OR TEST1 OR ESP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; Genome Res. 13:2265-2270(2003).
-!-FUNCTION: Could regulate proteolytic events associated with testicular germ cell maturation.
-!- SUBCELIULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUB=Cervical carcinoma;
MEDLINE=9923395; PubMed=10397266;
Hooper J.D., Nicol D.L., Dickinson J.L., Eyre H.J., Scarman A.L.,
Normyle J.F., Stuttgen M.A., Douglas M.L., Loveland K.A.,
Sutherland G.R., Antalis T.M.,
Trestisin, a new human servine proteinase expressed by premeiotic
testicular germ cells and lost in testicular germ cell tumors.";
Cancer Res. 59:3199-3205 (1999).
                                                                                                                                                               Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=20068805; PubMed=10600542;
Inoue M., Isobe M., Itoyama T., Kido H.;
"Structural analysis of esp-1 gene (PRSS 21).";
Biochem. Biophys. Res. Commun. 266:564-568(1999).
                                                                                                                                                                                                                                                                                                        Biochem. Biophys. Res. Commun. 252:307-312(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
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MEDLINE=20461760; PubMed=11004480;
                                                                                                                                                                                                                                                 MEDLINE=99045401; PubMed=9826525;
                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Eosinophil;
                                        STANDARD;
                                                                                                                                                                                                                                                                                           human eosinophils.";
                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                                                        NCBI_TaxID=9606;
                                        FEST HUMAN
                        FEST HUMAN
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Event=Alternative splicing; Named isoforms=3;

(Potential).

Name=1; Synonyms=L; IsoId=Q9Y6M0-1; Sequence=Displayed; Name=2; Synonyms=S;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009003; Cys_Gr_trypsin.
InterPro; IPR001234; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN JER; 1.
Hydrolase; Serine protease; Glycoprotein; Signal; GPI-anchor; Zymogen; Alternative splicing; Lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 AAPLSGP--CGRRVITSRIVGGEDAELGRWPWQGSLRLWDSHVCGVSLLSHRWALTAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC, .) (POTENTIAL).
N-LINKED (GLCNAC, .) (POTENTIAL).
N-LINKED (GLCNAC, .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27.4%; Score 534.5; DB 1; Length 314; 39.0%; Pred. No. 2.2e-35; ive 53; Mismatches 100; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED IN MATURE FORM (POTENTIAL)
               IsoId=Q9Y6M0-3; Sequence=VSP 005390;
TISSUE SPECIFICITY: Expressed predominantly in premeiotic
testicular germ cells, mostly late pachytene and diplotene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 AA; 34884 MW; E738CF73F6B56E98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60; GO:0005737; C:cytoplasm; TAS.
GO:0005624; C:membrane fraction; TAS.
GO: GO:0005886; C:plasma membrane; TAS.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform 2)
                                                                               spermatocytes.
SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP 005389
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                                                                                                                                                                                                                                                                                                           EMBL, AF058300, AAD41588.1, --
EMBL, AB01329; BAA85520.1; --
EMBL, AB031330; BAA85521.1; --
EMBL, AB031331; BAA89532.1, --
EMBL, AF058301; AAF79019.1; --
EMBL, AF058301; AAF79020.1; --
EMBL, AY558034; AAQ89393.1; --
HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:9485; PRSS21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.011; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222
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289
82
137
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33
67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 608159;
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Name=3;
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                                                                                                             202 GEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCOGDSGGPLVCEEGGRWFQAGIT 261
84 FETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY----LGNSPYDIA 139
                                                                               142 LIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mouse matriptase-2: identification, characterization and comparative mRNA expression analysis with mouse hepsin in adult and embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hooper J.D., Campagnolo L., Goodarzi G., Truong T.N., Stuhlmann H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Transmembrane protease, serine 6 (EC 3.4.21.-) (Matriptase-2).
                                                                                                                                                                                                                                                                                         262 SFGFGCGRRNRPGVFTAVATYEAWIRE---QVMGSEPGPAFP 300
                                                                                                                                                                                                                                                                                                                                          257 ŚWGVGCGRPNRPGVYINISHHFEWIQKIMAQSGMSQPDPSWP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             811 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J;
MEDLINE=22755759; PubMed=12744720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochem. J. 373:689-702(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quigley J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMS6 MOUSE
Q9DBI0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commerce entities requires a license agreement (see http://www.isb-sib.ch/annour or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Membrane anchored serine proteases: a rapidly expanding group of cell surface proteolytic enzymes with potential roles in cancer."; Cancer Metastasis Rev. 22:237-258(2003).
-!- FUNCTION: May play a specialized role in matrix remodeling processes in liver (By similarity).
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- TISSUE SPECIFICITY: Expressed at highest levels in liver, kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and uterus.

-!- DEVELOPMENTAL STAGE: Expressed at higher levels from 12.5 dpc to 15.5 dpc with a peak at 13.5 dpc. Expression in the developing liver as well as a restricted set of embrinic epithelial cells of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22668120; PubMed=12784999;
Netzel-Arnett S., Hooper J.D., Szabo R., Madison E.L., Quigley J.P.,
Bugge T.H., Antalis T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR009003; Cys_Ser_trypsin.
IPR002172; LDL_receptor_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001254; Peptidase_S1.
Interpro; IPR001314; Peptidase_S1A.
Pfam; PP00057; 1dl recept_a; 2.
Pfam; PP00089; trypsin; 1.
                         TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIMITS; PROUGS; CHYMOTRYPEIN.
PRINTS; PROUGEJ; LDINECEPTOR.
PROSITE; PSO11209; LDINA 1.
PROSITE; PS50068; LDINA 1; 1.
PROSITE; PS50068; LDINA 2; 3.
PROSITE; PS50049; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY240929; AAP69827.1; -. EMBL; AK004939; BAB23684.2; -. EMBL; BC029645; AAH29645.2; -. HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.308; -. MGD; MGD; MGI:1919003; TMPRSS6. InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
InterPro;
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us-10-037-417-46.rsp

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SEQUENCE FROM N.A.
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686
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MEDLINE=21133129, PubMed=11231276;
MEDLINE=2113229, PubMed=11231276;
Scarman A.L., Hooper J.D., Boucaut K.J., Sit M.-L., Webb G.C.,
Normyle J.F., Ancalis T.M.;
"Organization and chromosomal localization of the murine Testisin gene encoding a serine protease temporally expressed during
                                                                                                                                                                                                                                                                   38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                                                                                                                                                       98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP
                                                                                                                                                                                                                                                                                                                  158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN
                                                                                                                                                                                                                                                                                                                                                     218 LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEE-GGRWFQAGITSFGFGCGRRNRPGVF
                           SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;
                                                                                                                     SIMILARITY)
SIMILARITY)
                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                  12;
                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                  (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                27.3%; Score 533; DB 1; Length 811;
                                                                                                                                                                                                                                                 96; Indels
                                                                                                                                                                                                     -> PP (IN REF. 2).
32EB3E7C3127801B CRC64;
                                              EXTRACELLULAR (POTENTIAL)
                                                                                                          CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
CHARGE RELAY SYSTEM (BY
                                                                                                                                     N-LINKED (GLCNAC...)
                                                                        LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
SERINE PROTEASE.
                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                          Pred. No. 8e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Testisin precursor (EC 3.4.21.-) (Tryptase 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 AA.
                                                                                                                                                                                                                                      43.7%; Prec. ...
                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spermatogenesis.";
Eur. J. Biochem. 268:1250-1258(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEST_MOUSE STANDARD; 100JH4; 09JH77; 09DA14; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequing-mar-2004 (Rel. 43, Last annotation)
                                                                                                                                                                                                              90978 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  277 TAVATYEAWIRE 288
                                                                                                                                                                                                                                                                                                                                                                                                                                     797 TRVTRVINWIQQ 808
                                                                                                                                                                                                                                                  Matches 110; Conservative
                                                                                                                              762
1138
1184
216
338
433
518
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                                                                                                                                                                                                             811 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                     19
           Glycoprotein.
DOMAIN
                                                                                                                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                            ACT_SITE
CARBOHYD
                            TRANSMEM
                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                            ACT_SITE
                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                              CARBOHYD
                                                                                                                       SITE
                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRSS21.
                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                          DOMAIN
                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-21085660; PubMed=11217851;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Futunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Futunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Andota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Andota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T.,
Andota K., Matsuda H.A., Shinati M., Wangner I., Washio P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Achimi L.M., Staubli F., Suzuki R., Tomita M., Wangner I., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fulita M., Mariboldi M.,
Anonstein M.J., Bult C., Fletcher C., Fulita M., Mariboldi M.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Anordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sarauki H., Toyo-oka K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Printis, Process, trypsin; 1.

PRINTS; PROC722; CHYMOTRYPSIN.

SMART; SMO0020; Tryp SPC; 1.

PROSITE; PS50240; TRYPSIN DOX; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

Hydrolase; Serine procease; Glycoprotein; Signal; GPI-anchor; Zymogen;
STRAIN-BALB/C; TISSUE-Testis;
PubMed=11259427;
Wong G.W., ii., Madhusudhan M.S., Krilis S.A., Gurish M.F.,
Rothenberg M.E., Sali A., Stevens R.L.;
"Tryptase 4, a new member of the chromosome 17 family of mouse serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           testicular germ cell maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- DEVELOPMENTAL STAGE: Expressed in post-meiotic testicular germ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Belongs to peptidase family S1. CAUTION: Ref.3 sequence differs from that shown due to a stop codon in position 315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
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GO:0004252; F:serine-type endopeptidase activity; IDA.
Interpo; IPR009003; Cys_Sr_trypsin.
Interpro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK006271; -; NOT ANNOTATED CDS HSSP; P00763; 1DPO.
                                                                                                                                                                                                                                                                         Biol. Chem. 276:20648-20658(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF304012; AAK29360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY005145; AAG02255.1; -. EMBL; AF176209; AAF64407.2; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF226710; AAF64428.2;
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 3-324 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1916698; Prss21.
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                                                                                                                                                                                                                                              proteases.
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7;
                                                                                                                                                                                                                                                                                                                                        FMTNGTLEPAAEWSVLLGVHSQDGPLDG----AHTRAVAAIVVPANYSQVELGADLALLR 144
                                                                                                                                                                                                                                                                                                                                                       145 LASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEA 204
                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 MCNHMYKKP---DFRININGDMVCAGTPEGGKDACFGDSGGFLACDQDTVWYQVGWG
                                                                                                                                                                                                                                                                                                        SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                    205 TCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFG
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/Sv, and BALB/c;
MEDLINE=99452974; PubMed=10521469;
Worg G.W., Tang Y., Feyfant E., Sali A., Li L., Li Y., Huang C.,
Friend D.S., Krilis S.A., Stevens R.L.;
"Identification of a new member of the tryptase family of mouse and
human mast cell proteases which possesses a novel COOH-terminal
                                                                                                                                                (Potential).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
P -> H (IN REF. 3).
W, 56DC59884F3C3C04 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                              REMOVED IN MATURE FORM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tryptase gamma precursor (EC 3.4.21.-) (Transmembrane tryptase).
                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                           27.1%; Score 529; DB 1; Length 324; 38.1%; Pred. No. 6.1e-35; Live 53; Mismatches 97; Indels
                                                                                                                                       GPI-anchor amidated asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   265 FGCGRRNRPGVFTAVATYEAW----IREQVMGSEPGP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TESTISIN.
REMOVED IN MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AA
                                                                                                                 POTENTIAL.
                                                                                                      POTENTIAL.
                                                                                         POTENTIAL
                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                        36175 MW;
                                                                                                                                                                                                                                                        Best Local Similarity 38.19
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nydrophobic extension."
21
298
324
324
95
95
167
167
233
272
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177
210
283
275
324 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10090;
  22
239
239
295
248
248
244
214
244
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09QUL7;
                                                                                                                                                                                                                                                                                                                                         89
                                                                                                    DISULPID
DISULPID
DISULFID
                                                                                                                                                                                    CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                   43
                    CHAIN
PROPEP
ACT SITE
ACT SITE
ACT SITE
DISULFID
                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                         CARBOHYD
                                                                                           DISULFID
 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRYG_MOUSE
                                                                                                                                       LIPID
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@license.).
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rlausner R.D., Collins F.S., Wagner I., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Raha S.S., Locullan B., Garcia A.M., Gay L.J., Hullyk S.W.,

Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakeley R.W., Touchman J.W., Gren E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Recrigied Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16890312002).

"Insula SPECIFICITY: Expressed in many tissues.

"Insula SPECIFICITY: Expressed in many tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 LEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVE-------LGADLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79; Indels 41; Gaps
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(BY SIMILARITY).
(BY SIMILARITY).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
INTECHAIN (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 528.5; DB 1; Length 311; 41.6%; Pred. No. 6.4e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1349391; Tpsq1.
InterPro; IPR009003; Cys. Ser_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00144; TRYPSIN DOM; 1.
PROSITE; PS001134; TRYPSIN HIS; 1.
PROSITE; PS001135; TRYPSIN JER; FALSE_NEG.
Hydrolase; Serine protease; Signal; Glycoprotein; Zymogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRYPTASE GAMMA LIGHT CHAIN.
TRYPTASE GAMMA HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 N-LINKED (GLCNAC. . .) (PC
32656 MW; 7FC9D6EF6A2A8808 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF175760; AAF03698.1; -. EMBL, AF175523; AAF03696.1; -. EMBL; BC052325; AAH52325.1; -.
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311 AA;
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Best Local Similarity
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TRANSMEM
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ACT_SITE
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DISULFID
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X STGUINE=22388257; PubMed=12477932;

X Strausberg R.D., Feingold B.A., Grouse L.H., Derge J.G.,

X Alausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Alausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Backenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleton M., Soares M.B., Bonaldo M.F., Carawant T.L., Scheetz T.E.,

X Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R Wilting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length

R Munn and mouse coDA sequences.",

Thum and mouse coDA sequences.",

Thum and mouse coDA sequences.",
  ::::| |:|
---ELIVILSPHFSIVKRIIMYTGSPGPPGSSGDIA 119
                                         201
                                                                                                261
                                                                                                                        DVKTCSOAYNSP---NGSL-IQPDMLCA---RGPGDACQDDSGGPLVCQVAGTWQQAGVV 232
                                                          GEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGIT
                                        LIRIASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
-! - SUBCELLULAR LOCATION: Type II membrane protein (Probable).
-! - TISSUE SPECIFICITY: Highly expressed in intestine, kidney, lung, and thymus. Not expressed in skeletal muscle, liver, heart, testis and brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C., Schwartz R.H.; "Cloning and chromosomal mapping of a gene isolated from thymic stromal cells encoding a new mouse type II membrane serine protease, epithin, containing four LDL receptor modules and two CUB domains."; Immunogenetics 49:420-428(1999).
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                           [1] -
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE C.B.158CUE_Thymus;
MEDLINE=99216460; PubMed=10199918;

Wim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C.,

"im M.G., a gene isolated from '
                                                                                                                                                                                                                                                                                      10-0CT-2001 (Rel. 40, Last sequence update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Epithin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN~C.B.17SCID; TISSUE=Thymus;
Kim M.G., Chen C., Cho E.G., Park D., Schwartz R.H.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVISIONS TO 23; 321; 325; 343; 409-410 AND C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                                                                                        855 AA
                                                                                                                                                      SFGFGCGRRNRPGVFTAVATYEAWIREQV 290
                                                                                                                                                                     (Rel. 38, Created)
(Rel. 40, Last seq
(Rel. 42, Last ann
                                                                                                                                                                                                                                                        STANDARD;
  : :::: | ||
VN-SSDYQVHLG-
                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                15-JUL-1999
16-OCT-2001
10-OCT-2003
                                                                                                                                                                                                                                                       ST14 MOUSE
P56677;
                                                                                                                          180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 CGGSLIAPSWVLSAAHCFM--TNGTLEPAAEWSVLLGVHSQD-GPLDGAHTRAVAAIVVP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 CGASLISPDWLVSAAHCEQDDKNEKYSDYTMWTAFLGLLDQSKRSASGVQELKLKRITH 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease; Transmembrane; Repeat.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 4 LDL-receptor class A domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4F10E84DA2146DD5 CRC64;
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EXTRACELIULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                       MGD; MGI:1338881; St14.
GO; GO:0005576 C:extracellular; IDA.
GO; GO:009897; C:extrinsic to plasma membrane; IDA.
GO; GO:0008236; F:serine-type peptidase activity; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .) (GLCNAC. . .)
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.8%; Score 523; DB 1; 39.5%; Pred. No. 5.3e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000839; CUB.
InterPro; IPR000803; CVB.
InterPro; IPR000803; CVS. Errypsin.
InterPro; IPR000172; LDL receptor A.
InterPro; IPR001214; Peptidase_SIA.
InterPro; IPR001314; Peptidase_SIA.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
Pfam; PF00431; CUB; 2.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00192; LDLB; 4.
SMART; SM00192; LDLB; 4.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; LDLB; 4.
PROSITE; PS01180; LDLB; 4.
PROSITE; PS01180; LDLB; 4.
PROSITE; PS01180; LDLB; 4.
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855 AA;
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CARBOHYD
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                                                                            129 ANYSQVELGADLALLRIASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
                                                           LPWVLQEVELRLLGEATCQCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
Mitsui S., Okui A., Kominami K., Yamaguchi N.;
"Cloning and characterization of a novel serine protease, mBSSP-4.";
Submitted (JAN-1998) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family Sl.
                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

MCBI_TaxID=10090;
                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Brain-specific serine protease 4 precursor (EC 3.4.21.-) (BSSP-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRAIN-SPECIFIC SERINE PROTEASE 4.
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (POTENTIAL) FBBF03C0C285E7E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.4%; Score 516; DB 1; Length 306; 37.1%; Pred. No. 6.2e-34; ive 47; Mismatches 118; Indels 2
                                                                                                                       248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
                                                                                                                                         CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                  306 AA
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Pfam, PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PKOSITE; PS00135; TRYPSIN_SER; 1.
PKOTORIE; PS00135; TRYPSIN_SER; 1.
SIGNAL
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Interpro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB010778; BAB20262.1; -. HSSP; P00763; 1DPO.
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                                                                                                                                                                                                                                    STANDARD;
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306
90
141
242
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                    BSS4 MOUSE
Q9ER10;
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Gaps

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Best Local Similarity Matches 109; Conserv

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                                                                                                                                                                                                        238
                                                                                                                                                                                                                                                                                                 60 WQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGAHT 119
                                                                                                                9 PGQLGAVANSDSYSLYGL------VPSGPARGPPYCGRPEPSARIVGGSNAQPGTWP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89352460; PubMed=2504277;
MEDLINE=89352460; PubMed=2504277;
Wanderstlice P., Craik C.S., Nadel J.A., Caughey G.H.;
Wanderstlice P., Craik C.S., Nadel J.A., Caughey G.H.;
Wolecular cloning of dog mast cell tryptase and a related protease:
structural evidence of a unique mode of serine protease activation.";
Biochemistry 28:4148-4155(1989).
-: FUNCTION: Tryptase is the major neutral protease present in mast
cells and is secreted upon the coupled activation-degranulation
response of this cell type.
-: CATMATTIC ACTIVITY: Preferential cleavage: Arg-|-, Lys-|-, but
with more restricted specificity than trypsin.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
-: SUBUNIT: Homotetramer.
                                                                                                                                                                                                                                                                         179 GDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDT
                               7 PPALG----GDQFSILILIVILISTAPISAATIRVSPDCGKPQQLNRIVGGEDSMDAQWP
                                                                                                                                                                                 120 RAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGW
                                                                                                                                                                                                                                                                                                                                                               239 COGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                                                         mast cell activation.
SIMILARITY: Belongs to peptidase family S1. Tryptase subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canıs ramılarıs (109).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS, SO1.143; ...

InterPro; IPR001254; Peptidase S1.

InterPro; IPR0012154; Peptidase S1.

InterPro; IPR001214; Peptidase S1.

InterPro; IPR001214; Peptidase S1.

InterPro; IPR001214; Peptidase S1A.

PRINTS; PR00722; CHYWOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00134; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN S1A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tryptase precursor (EC 3.4.21.59)
Canis familiaris (Dog).
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HSSP; P20231; 1AAO.
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80 SWVLSAAHCFMTNGTLEPAAEWSVLL---GVHSQDGPLDGAHTRAVAAIVVPANYSQVEL 136
                                                                                                                                                                                                                                                                                                                                            137 GADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEV 196
                                                                                                                                                                                                                                                                                                                                                                                                           119 GADIALLELEDPVNVSAHVQPVTLPPALQTFPTGTPCWYTGWGDVHSGTPLPPPFPLKQV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 ELRILGEATCQCLYSQPGPFNLTLQILPG-----MLCAGYPEGRRDTCQGDSGGPLVC 249
                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                       12 İGSLÜVEVSPAP-----GQALQRVGIÜGGREAPGSKWPWQVSLRLKGQYWRHICGGSLIHP 66
                                                                                                                                                                                                                                                            23 LYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGG---GHICGGSLIAP
                                                                                                                                                                                               Query Match 26.3%; Score 514.5; DB 1; Length 275;
Best Local Similarity 42.2%; Pred. No. 7.2e-34;
Matches 124; Conservative 27; Mismatches 100; Indels 43; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 RVRGVWLQAGVVSWGEGCAQPNRPGIYTRVAXYLJDWIHQYV------PKEP 275
ACTIVATION PEPTIDE (BY SIMILARITY).
TRYPTASE.
CIRAGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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BY SIMILARITY.
BY SIMILARITY.
N'INKED (GLONAC. . .) (POTENTIAL).
M; C3B869251F248D5B CRC64;
                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
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Search completed: February 25, 2004, 15:47:56 Job time: 52 secs

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February 25, 2004, 15:36:03 ; Search time 84 Seconds
(without alignments)
1340.952 Million cell updates/sec
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1953
1 MAÇKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                            1017041 seqs, 315518202 residues
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *plant:*
sp_roden:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                       sp archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rvirus:*
sp_bacteriap:*
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sp_phage:*
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                              SPIREMBL 25:*
                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                              Searched:
                                                                                                                                                             Sequence:
                                                                             Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8nby4 homo sapien	Q99144 mus musculu	Q8bjv6 mus musculu		Q80x17 mus musculu	Q8rla6 mus musculu	Q8nf86 homo sapien	Q8n171 homo sapien	Q96rz8 homo sapien	Q8bjr6 mus musculu	Q9pvx7 xenopus lae	Q7t0x2 xenopus lae	088781 rattus ratt	Q9dgr3 xenopus lae	Q8wvcl homo sapien	Q9bye2 homo sapien
SUMMARIES	D	Q8NBY4	Q99L44	QBBJV6	QBOWM7	Q80X17	QBR1A6	QBNF86	Q8N171	Q96RZB	QBBJR6	Q9PVX7	Q7T0X2	088781	Q9DGR3	QBWVCl	Q9BYE2
	DB	4.	11	11	11	11	11	4	4	4	11	13	13	11	13	4	4
	Query Match Length DB	766	339	340	277	331	331	284	327	321	328	389	320	297	317	422	581
d(Query Match	61.5	32.3	31.4	30.9	30.9	30.7	30.2	30.2	29.8	29.2	29.0	28.7	28.7	28.6	27.6	27.6
	Score	1202	630.5	613	603	603	009	590	590	582	570	567	561	560.5	558	540	540
	Result No.		2	ť	4	ιΩ	9	7	80	σ	10	11	12	13	14	15	16

Q7tml0 mus musculu Q86ym4 homo sapien Q86ym4 homo sapien Q86ym2 trtus norv Q91j17 rattus norv Q91j17 rattus norv Q80yd8 mus musculu Q81j20 mus musculu Q91x9 mus musculu Q91x9 mus musculu Q7x11 homo sapien Q9xm1 ovis aries Q812a6 mus musculu Q9413 mus musculu Q94143 mus musculu Q1272 xenopus eu Q42772 xenopus eu	QBVIE2 mus musculu Q96rz6 homo sapien Q604pl cavia porce Q95me7 oryctolagus Q97506 sus scrofa Q8r0p5 mus musculu
Q7TMLQ Q86YM4 Q98YE1 Q80YZ3 Q80YD1 Q80YD8 Q8CFE0 Q9CYZ4 Q9BYKC4 Q9BYKC4 Q9BYKC4 Q9BYKC4 Q9BYKC4 Q9DYZ9 Q9CXZM1 Q9DAT3 Q9DAT3 Q9DAT3 Q9DAT3 Q9DAT3 Q9DAT3 Q9DAT3 Q9CAT4 Q9C	Q8VIF2 Q86RZ6 Q60491 Q95ME7 Q97506
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307 358 358 358 311 855 311 205 205 205 205 205 205 205 205 205 205	335 275 421 624 643 638
72222222222222222222222222222222222222	4444444 644444444444444444444444444444
538.5 538.5 538.5 537.5 530.5 523 523 523 523 523 523 523 523 523 52	474.5 473.5 472.5 470.5 469
11 11 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	4 4 4 4 4 4 10 H G W 4 R

ALIGNMENTS

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RESULT 1

OBNEY4

DECT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2003 (TrEMBLrel. 22, Last sequence update)

DE Mypothetical protein FLJ90661.

SHAPOTHAGIAN WELLAR (Tremble FLJ90661.

SHAPOTHAGIAN (Tremble FLJ90661.

NAMBLAGIAN (TREMBLRE) FRIMARES; Catarrhini; Hominidae; Homo.

NICH TAXID=9606; Maranis Primates; Catarrhini; Hominidae; Homo.

NICH TAXID=9606; Maranis Primates; Catarrhini; Hominidae; Homo.

NICH TAXID=9606; Maranis Maran
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1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSG-PARG-PPYCGRP-EPSARIVGGSNAQ-PG
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                                                                                                                                                                                                                                                                                                                     90 MTNGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA 149
                                                                                                                                                                                                                      61 SLGPAVMPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL 120
                                                                                                                                                                                                                                                                                       269
                                                                                                                                 1 MINGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPA 60
                                                                                                                                                                                        SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQBVBLRLLGBATCQCL
                                                                                                                                                                                                                                                                                     YSQPGPFNLTLQ1LPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAG1TSFGFGCGR
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane-associated serine protease of the gamma-tryptase/prostasin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ, and Swiss; TISSUE=Lung; Verghese G.M., Caughey G.H.; "Molecular cloning and characterization of mouse prostasin, a type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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0
61.5%; Score 1202; DB 4; Length 766; ilarity 100.0%; Pred. No. 2.1e-88; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kitamura K., Takefumi N., Kimio T.;
"mouse serine protease.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; BC003851; AAH03851.1; -.
EMBL; AR378086; AAL065120.1; -.
EMBL; AR378086; AAL06519.1; -.
EMBL; AB03844; BAB82496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene family.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PERMY PRO009; trypsin; 1.

PRINTS: PR0072; CHYMOTRYPSIN.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS0240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN LIS; 1.

PROSITE; PS00135; TRYPSIN LIS; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 339 AA; 36216 MW; BC2DE88BC057AF10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    270 RNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0004263; R:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; R:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similar to protease, serine, 8 (Prostasin) PRSS8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001314; Peptidase_S1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1923810; Prss8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                               220;
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  Query Match
                             Local
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                           Best Loca
Matches
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Q99L44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 ACQGDSGGPLSCPMEGIWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV--AELQP 290
                                                                                                                                                                                                                                                                                                                                                                                                              56 WPWQVSITYDGNHVCGGSLVSNKWVVSAAHCFPREHSRE---AYEVKLGAHQLDSYSNDT 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 VVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 WGDVQEADPLPLPWVLQEVELRLIGEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 TCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGP 297
                                                                                                                                                                                                                                                                                                                                                           58 WPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDGA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
                                                                                                                                                                                    1 MAQKGVLGPGQLGAVANSDSYSLYGLVPSG-PARG-PPYCGRP-EPSARIVGGSNAQPGT 57
                                                                                                                                                                                                                                                                   1 MALRVGLGLGGLEAVT---ILLLLGLLQSGLRADGTEASCGAVIQP--RITGGGSAKPGQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 18;
         Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 RVVPQTQESQPDGHLCNHHPVFSSAAAPKLLRPVLFLPLGLTLGLLSL 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 AFPTQPQKTQSD---CLHQTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.4%; Score 613; DB 11; Length 340; 41.5%; Pred. No. 2.2e-41; tive 46; Mismatches 140; Indels 10
                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
         DB 11;
    32.3%; Score 630.5; DB 11;
41.7%; Pred. No. 8.7e-43;
ttive 48; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 23, (TrEMBLrel. 23, I
Query Match
Best Local Similarity 41.7%
Matches 145; Conservative
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01-MAR-2003
01-OCT-2003
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Matches 145;
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26

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253 ALPNRPGVYINVAKYSPWIQARL 275
                                                                                                                                      268 GRRNRPGVFTAVATYEAWIREQV 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 129; Conservative
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01-JUN-2002
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01-JUN-2003
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Best Local S
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Q8R1A6;
                                                                                                                                                                                                                                                                                                        RESULT 5
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                                                                                                TWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLDG 116
                                                                                                                                   176
                                                                                                                                                                                                                                                                                              113 TVVHTVAQIITHSSYREEGSQGDIALIRLSSPVTFSRYIRPICLPAANASFPNGLHCTVT 172
                                                                                                                                                                                                                                                                                                                                                            GWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRR 236
                                                                                                                                                                                                                                                                                                                                                                                                      |||| : | | || || :| | GWGHVAPSVSLQTPRPLQQLEVPLISQENTIQQDMLCAGYVKGGK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AAEWSVLLGVHSQDGPLDGAHTRAVAA--IVVPANYSQVELGADLALLRLASPASL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 GPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 PAFPTOPOKTOSD---CLHOTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V [1]

P SEQUENCE FROM N.A.

STRAIN-BALB/c; TISSUE-Testis;

A Wong G.W., Yasuda S., Li L., Stevens R.L.;

Wong G.W., Yasuda S., Li L., Stevens R.L.;

"Cloning and characterization of mouse tryptase-6 (wT6).";

R Woll GO:0004263; F:chymotrypsin activity; IEA.

R GO: GO:0004263; F:chymotrypsin activity; IEA.

R GO: GO:0004269; F:trypsin activity; IEA.

R GO: GO:0004269; P:proteolysis and peptidolysis; IEA.

InterPro: IPR0010254; Peptidase_SIA.

"InterPro: IPR001134; Peptidase_SIA."
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PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp SPc; 1.
PROSITE; PS50240; TRYPSIN DDM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
SEQUENCE 277 AA; 29887 MW; 3310C067573E5E74 CRC64;
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Last annotation update)
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46.4%; Pred. No. 1.1e-40;
tive 30; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tryptase-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 AAEWSVILG-VHSQDGPLDGAHTRAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 LPVCLPKPGDPLDPGTMCWVTGWGHIGTNQPLPPPFTLQBLQVPLIDAETCNTYYQENSI
                                              196 VGANVPQGERI----VLPGNLCAGYRRGHKDACQGDSGGPLTCMESGHWVLVGVVSWGKGC
211 ---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Muš musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SEQUENCE FROM N.A.

STRAIN-BALB/c; TISSUE=Brain;

Nong G.W., Yasuda S., Stevens R.L., Li L.;

Wong and characterization of mouse tryptase-5 (mT5).";

Submitted (MAR.2003) to the EMBL/GenBank/DDBJ databases.

R MSD, AP266139; AAP23216.1; -.

EMBL, AY266139; AAP23216.1; -.

EMBL, AY266139; AAP23216.1; -.

EMBL, AY266139; AAP23216.1; -.

EMBL, AY266139; AP2616.1; -.

EMBL, AY266139; Firthysin activity; IEA.

GO; GO:00004295; Firthysin activity; IEA.

R O; GO:0004295; Firthysin activity; IEA.

R D(GO:0006208); Privecelysis and peptidolysis; IEA.

InterPro; IPR001314; Peptidase_S1A.

R Pfan; PF00089; trypsin; 1.

R PROSITE; PRO040; Tryp.SPC; 1.

R PROSITE; PS0040; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 331;
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(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last sequence update)
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PRINTS, PR00722, CHYMOTRYPSIN.
SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 AAEWSVILIG-VHSQDGPLDGAHTRAVAAIVVPANYSQVE-LGADLALLRLASPASLGPAV 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 -SIYTVLLGTISSYPEDNEFKELRAVAQFIKHPSYSADEHSSGDIALVQLASPISFNDYM 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 WPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQ--- 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 LPVCLPKPGDPLDPGTMCWVTGWGHIGTNQPLPPPFTLQBLQVPLIDABTCNTYYQBNSI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                38 CGRPBPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  Length 331;
                                                                                                                                                                                                                                                                                                                                                                                              30.7%; Score 600; DB 11; Length 3:
43.5%; Pred. No. 2.4e-40;
tive 39; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Darrow A.L., Qi J., Andrade-Gordon P., Chen C., "DNA encoding the human serine protease EOS."; Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                             Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            PERINTS PRO0089; LTYPSin; 1.

PRINTS, PR00722; CHYMOTRYPSIN.

PROSITE; PS0040; TTYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

PROSITE; PS00135; TRYPSIN HIS; 1.

Hydrolase; Protease; Serine protease.

SEQUENCE 331 AA; 35639 MW; C06FGEF2FA261636 CRC64;
                                                                                                                                                                HSSP, P00761; IANI.
MGD; MGT:1917064; 2010001P08Rik.
GG; GG:0004263; F:chymotrypsin activity; IEA.
GG; GG:0008233; F:peptidase activity; IEA.
GG; GG:0008235; F:peptidase activity; IEA.
GG; GG:0008236; F:peptidase activity; IEA.
GG; GG:0006269; F:properolysis and peptidolysis; IEA.
InterPro; IPR01254; Peptidase_SI.
InterPro; IPR001254; Peptidase_SIA.
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) RIKEN CDNA 2010001P08 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            284 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBNF86;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                        EMBL; BC024903; AAH24903.1;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.5%
Matches 128; Conservative
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SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                                           NCBI TaxID=10090;
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                                                                                                                    TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSNFB6
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QBNF86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 GPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 CGQPRMSSRIVGGRDGERPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRAL---
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
             EMBL, AESSGABA, AANO4055.1; ...

REMBL, AESSGABA, AANO4055.1; ...

RO; GO:0008233; F:chymotrypsin activity; IEA.

RO; GO:0008239; F:peptidase activity; IEA.

RO; GO:0006208; F:trypsin activity; IEA.

RINCERPO; IPRO0003; Cys Ser trypsin.

RINCERPO; IPRO0134; Peptidase_S1.

R PRONTS; PRO0134; Peptidase_S1A.

R PROSITE; PSO0134; TRYPSIN DOM; 1.

R PROSITE; PSO0134; TRYPSIN DOM; 1.

R PROSITE; PSO0134; TRYPSIN DOM; 1.

R PROSITE; PSO0134; TRYPSIN HIS; 1.

R PROSITE; PSO0135; TRYPSIN FIR; 1.

R PROSITE; PSO0135; TRYPSIN FIR; 1.

R PROSITE; PSO0135; TRYPSIN FIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99; Indels
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Strausberg R.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protease, serine, 8 (Prostasin) (Fragment).
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GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR00903; Cys Ser trypsin.
InterPro; IPR001234; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
30.2%; Score 590; DB 4;
Best Local Similarity 46.3%; Pred. No. 1.3e-39;
Matches 119; Conservative 29; Mismatches 99;
BELONGS TO PEPTIDASE FAMILY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2003 (TrEMBLrel. 25,
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us-10-037-417-46.rspt

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Best Local Similarity
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                               128;
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                               Matches
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                                                                                                                                                                                                                                                                                                                                        98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 GPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP
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Hum. Mol. Genet. 10.339-352(2001).

-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL, AR006466; AAX61269.1;

HSSP: P00761; 1AN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                            10;
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Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
Higgs D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 321;
                                                                                                                                                                          Length 327;
                                                                                                                                                                                                                                         99; Indels
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SEQUENCE 321 AA; 33829 MW; FFF5089EDC4FC73D CRC64;
                                                                                                                    327 AA; 35106 MW; 60458ED817AC1CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0004253; F:chymotrypain activity; IEA.
GO; GO:0004235; F:ceptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR001054; Peptidase_SIA.
InterPro; IPR001254; Peptidase_SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
HS transmembrane tryptase, gene name TMT, AF175522_
                                                                                                                                                                             30.2%; Score 590; DB 4; 46.3%; Pred. No. 1.5e-39;
                                                                                                                                                                                                                                         29; Mismatches
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PRINKS; PR00722; CHYMOTRYPSIN.
MART; SM00020; TryP_SPC, 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVFTAVATYEAWIREQV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVYTSVATYSPWIQARV 325
                                                                                                                                                                                                                                         Matches 119; Conservative
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                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                 SEQUENCE
                                                                                                                                                                                Query Match
                                                                                  NON TER
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Score 582;

29.8%;

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 PYCGRPEPS---ARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTN 92
                                                                                                                                                                                              81
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length oDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                          82 GSLN-SSDYQVHL-----GELEITLSPHFSTVRQIILHSSPSGQPGTSGDIALVELSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 DY--PGPGGSILQ--PDMLCA---RGPGDACQDDSGGPLVCQVNGAWVQAGIVSWGEGCG
                                                                                                                                                                 24 PGCGRPQVSDAGGRIVGGHAAPAGAWPWQASLRIRRVHVCGGSLLSPQWVLTAAHCF--S
                                                                                                                                                                                                                                                                                                                                                                                                                                      149 ASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 LYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG
                                         Gaps
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J. Biol. Chem. 5:3363-3371(2003).

EMBL; AKO80201; BAC37864.1; --

EMBL; AX162410; AA017162.1; --

EMBL; AF542056; AA027572.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAR-2003 (TremBirel. 22, Last sequence update)
01-OCT-2003 (TremBirel. 25, Last annotation update)
Similar to MARAPSIN precursor (Channel-activating protease 2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6; TISSUE=Bladder;
MEDLINE=22439795; PubMed=12441343;
Bhagwandin V.J., Hau L.W., Mallen-St Clair J., Wolters P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brathwaite M., Waeltz P., Schlessinger D., Nagaraja R.; "Genomic Sequence Analysis in the Mouse T-complex Region."; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                         87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI2450123; Mpn.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys. Ger_trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 RRNRPGVFTAVATYEAWIREQVM---GSEPGPAFPTQP 303
46.0%; Pred. No. 6.6e-39;
live 35; Mismatches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003
                                                                        Matches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiative
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                                                                                                                                                                                                                                                                                                                            190 DIPKCNILYNKDVESDFQLKTIKDDMLCAGFAEGKKDACKGDSGGPLVCLVDQSWVQAGV 249
                                                                                                                                                                                                                                                                                                                                                              261 TSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSE-PGPAFPTQPQK------TQSD 309
                                                                                                                                                                                                                                                              LLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                              83
                                                                                                                                                                                    15 ILRSGTEGARTLRACGHPKMFNRMVGGENALEGEWPWQVSIQRNGIHFCGGSLIAPTWVL 74
                                                                                                                                                                                                              SAAHCFMINGILEPAAEWSVILGVHSQDGPLDGAHTRAVAAIVVPAN--YSQVELGADLA
                                                                                                                                                                                                                                                                                                              202 GEATCOCLYSQPGPFNLTLQ-ILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGI
                                                                                                                                                              26 LVPSGP--ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVL
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                      22;
                                                                                                              Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'The expression control of xepsin by non-axial and planar
                                                                                                            29.2%; Score 570; DB 11; Length 3 41.3%; Pred. No. 6.2e-38; cive 38; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                posteriorizing signals in Xenopus epidermis.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-! SINILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; ABO18894; BAA84941.1;
HSSP; PO0763; 1DPO.
                                                                                     328 AA; 35789 MW; DC0B20F1AB3EB840 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0004263; F:chymotrypsin activity; IEA.
GO: GO:0008233; F:chymotrypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR003003; Cys Ser_trypsin.
InterPro; IPR001254; Peptidase_SI.
InterPro; IPR00134; Peptidase_SI.
Pfem; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Epidermis specific serine protease
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS50240; TRYPSIN DM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN HIS; 1.
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SMART; SM00020; Tryp, SFC; 1.
PROSITE; PS50240; TRYPSIN DOW; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              310 CLHQTAF-LDSARILLR 325
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                                                                                                                                        Conservative
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                                                                                                                       Local Similarity
hes 131; Conserv
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SEQUENCE FROM N.A.
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                                                                            Protease.
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                                                                                      SEQUENCE
                                                                                                               Query Match
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Attaubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altaubner R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Sares M.B., Bonaldo M.F., Casrainci P., Frange C.,
Brownstein M.J., Usdin T.B., Toophiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rosak S.A., McZwan P.J., McKernan R.J., Malke J.A., Gunzarne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
McGeneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 LTLQILP-----GMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRR 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VSYYTVYLGAYQLSAPDNSTVSRGVKSITKHPDFQYEGSSGDIALIELEKPVTFTPYILP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
                                                                                                                                                                                                                                                                                                 38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                           20;
                                                                                                                                                29.0%; Score 567; DB 13; Length 389; 40.2%; Pred. No. 1.3e-37; arive 45; Mismatches 97; Indels 20
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 389 AA; 42375 MW; B31FB4A2F5D1F6E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 NRPGVFTAVATYEAWIREQV---MGSEPGPA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 NRPGVYTKVQYYQDWLKTNVPLIVFSEEGPS 277
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Xenopus laevis (African clawed frog)
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MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                               Conservative
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NCBI_TaxID=8355;
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Similarity
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01-OCT-2003
                                                                                                  Query Match
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Q9DGR3
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                                                                                                                                                                                                                                                                           FNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGV 275
                                                                                                                                                                                                                                                                                                                                                       FTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSDCLHQTAFLDSARI-----LLR 325
                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                     SARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSV
                                                                                                                                                                                  3 SERIVGGTDSXKGEWPWQISLSYKGEPVCGGSLIANSWILTAAHCFDS----QNVSQYKV
                                                                                                                                                                                                                   104 LLGVHSQDGPLDGAHT--RAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLP
                                                                                                                                                                                                                               ----ilddmrcagykegkidacogdbsggriyckvnnrwwgygivswgigcggangegv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                 Gaps
                                                                                                                       28.7%; Score 561; DB 13; Length 320; 37.3%; Pred. No. 3.2e-37; ative 55; Mismatches 107; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Fisher; TISSUB=Brain;
MEDLINE=9889725; pubMed=9722524;
Davies B.J., Pickard B.S., Steel M., Morris R.G., Lathe
"Serine Proteases in Rodent Hippocampus.";
J. Baol. Chem. 273:23004-23011(1998).
EMBI; AJ005642; CRA06644.1; -.
HSSP; P00763; 1DPO.
                                                    Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56000; AAH56000.1; -.
Hypothetical protein
SEQUENCE 320 AA, 35275 MW; ODC924A312AFA375 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; S01.252; -... GO; GO:0004263; F:chymotrypsin activity; IEA. GO; GO:0004263; F:chymotrypsin activity; IEA. GO; GO:0006295; F:trypsin activity; IEA. GO; GO:006508; P:proteolysis and peptidolysis; IEA. InterPro; IPR009003; Cys. Ser_trypsin. InterPro; IPR001254; Peptidase_S1. InterPro; IPR001314; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine protease precursor (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT:
                                                                                                                                                                                                                                                                                                                                                                                                                    292 ALGGGADNQARSHLTISLS 310
                                                                                                                                                                                                                                                                                                                                                                                                     326 PL-----SHISVGVS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPc; 1.
 mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus rattus (Black rat).
                                                                                                                                               Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                         Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 LGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQE 195
                                                                                                                                                                                                                                                                                                                                             9/
                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 VELRILGEATCOCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRW
                                                                                                                                                                                                                                                                                                                                             22 SLYGLVPSGPA-----RGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MADDMed=10903452;
MEDLINE=2033741; PubMed=10903452;
**Eamada K., Takabatake T., Takeshima K.;
**Isolation and characterization of three novel serine protease genes
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                    28.7%; Score 560.5; DB 11; Length 297; 39.4%; Pred. No. 3.3e-37; vative 47; Mismatches 110; Indels 11;
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                                                                                                                                 SIGNAL <1 23 POTENTIAL.
CHAIN 24 297 SERINE PROTEASE.
SEQUENCE 297 AA; 32086 MW; 6DA25C6633D6AB55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Xenopus laevis.";

Gene 252:209-216(2000).

EMBL. ABG98496; BAB08216.1; -.

HSSP, P00763; 1DPO.

MEROPS; S01.048; -.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0008235; F:peptidase activity; IEA.

GO; GO:0006289; F:trypsin activity; IEA.

GO; GO:0006588; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 16, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 FOAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 LLTGIISWGEGCAERNRPGVYTSLLAHRPWVQRIVQG 281
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
Hydrolase; Protease; Serine protease; Signal.
SIGNAL 123 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro, IPR009003, Cys_Ser_trypsin.
InterPro, IPR001254; Peptidase_S1.
InterPro, IPR001314; Peptidase_S1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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PRINTS; PR00722; CHYMOTRYPSIN.
PRART; SM00020; Tryp_SPc; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
PHYDOLASE; PF00125; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                           Matches 109; Conservative
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                                                                                                                                                       91 INGTLEPAAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPAS 150
                                                                                                                                                                              211 SOPGPFNLT-LOILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGR 269
                                                                           35 PPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCF----M 90
                                                                                                  29 PPLCGSPVFSSRIVGGTDTRQGAMPWQVSLEFNGSHICGGSIISDQMILTATHCIEHPDL 88
                                                                                                                                                                                                                                       151 LGPAVWPVCLPRASHRFVHGTACWATGWGDVQBADPLPLPWVLQEVELRLLGEATCQCLY
                                                                                                                                                                                                                                                                                                                                                                                             270 RNRPGVFTAVATYEAWIREQ-VMGSEPGPAFPTQPQKTQSDCLHQTAFLDSARILL 324
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
Query Match 28.6%; Score 558; DB 13; Length 317; Best Local Similarity 39.2%; Pred. No. 5.6e-37; Matches 116; Conservative 45; Mismatches 119; Indels 16;
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27.6%; Score 540; DB 4; Length 422;
Best Local Similarity 40.2%; Pred. No. 2.1e-35;
Matches 113; Conservative 39; Mismatches 95; Indels
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NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; EC018146; AAH18146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R HSEP: POOTESTAND AMELET S. F. FREELY F. F. FREELY FOOTESTAND.

R GO; GO:0008235; F:chymotrypsin activity; IEA.

GO; GO:0008235; F:chymotrypsin activity; IEA.

R GO; GO:0008235; F:crypsin activity; IEA.

R GO; GO:0006508; F:crypsin activity; IEA.

R InterPro; IPR00137; IDL_receptor A.

InterPro; IPR00137; IDL_receptor A.

InterPro; IPR001314; Peptidase_S1.

R InterPro; IPR001314; Peptidase_S1.

R PRIMTS; PR00757; Idl_recept_a; 4.

R PRIMTS; PR00757; Idl_recept_a; 4.

R PRIMTS; RN00192; CHMUGTRYBSIN.

R RMART; SN00192; IDLa; 4.

R PROSITE; PS00068; IDLRACEPTOR.

R PROSITE; PS001309; IDLRACEPTOR.

R PROSITE; PS001309; IDLRACEPTOR.

R PROSITE; PS001309; IDRA_1; 2.

R PROSITE; PS001309; IDRA_1; 2.

R PROSITE; PS001309; IDRA_1; 2.

R PROSITE; PS001309; INRA_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422 AA
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Q8WVC1;
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Gaps

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148 SKĠNPECDGKEDCSDGSDEKDCDCGLRSFTRQARVVĠĠTDADEĠEWPWQVSLHALGQGHI 207
                                                           72 CGGSLIAPSWVLSAAHCFWTNG--TLEPAAEWSVLLGVHSQ-DGPLDGAHTRAVAAIVVP 128
                                                                                 129 ANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
71
                                                                                                                                              189 LPWVLQEVELRLLGERICQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL-
----SARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                                                           248 VCEEGGRWFQAGITSFGFGCGRRNRFGVFTAVATYEAWIRE 288
                                                                                                                                                                                                                                                                            378 SVEADGRIFQAGVVSWGDGCAQRNKFGVYTRLPLFRDWIKE 418
     32 ARGPPYCGRPEP-
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TIVE: AMINO ACIU
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TOPOLOGY: linear
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Sequence 7, Appli
Sequence 9, Appli
Sequence 12, Appl
Sequence 11, Appl
Sequence 263, Appl
Sequence 263, Appl
Sequence 263, Appl
Sequence 263, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 257, Appl
Sequence 6, Appli
Sequence 6, Appli
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Sequence 21, Appl
Sequence 2, Appli
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                                                                                             February 25, 2004, 15:45:03; Search time 44 Seconds (without alignments) 418.874 Million cell updates/sec
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Sequence 6, Ar
Sequence 9, Ar
Sequence 26,
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Sequence 10,
                                                                                                                                                              US-10-037-417-46
1953
1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4,
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1. /cgn2 6/ptodata/2/iaa/5A_COMB.pep:*
2. /cgn2 6/ptodata/2/iaa/5B_COMB.pep:*
3. /cgn2 6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2 6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2 6/ptodata/2/iaa/PerTUS_COMB.pep:*
6: /cgn2 6/ptodata/2/iaa/PerTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-386-642-11

US-09-386-642-11

US-09-907-794A-263

US-09-907-775A-263

US-09-007-125A-263

US-09-027-337-2

US-09-627-337-2

US-09-627-337-2

US-09-627-337-2

US-09-627-337-2

US-09-902-775A-257

US-09-386-623A-9

US-09-654-600-10

US-09-654-600-10

US-09-654-600-10

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Maximum Match 100%
Listing first 45 summaries
                                                                 OM protein - protein search, using sw mode]
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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No.
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Sequence 5, Appli	Sequence 65, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 53, Appl	Sequence 19, Appl		Sequence 21, Appl		Sequence 4, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 7, Appli	Sequence 6, Appli	Sequence 1, Appli	Sequence 3, Appli
US-08-978-404B-5	US-08-944-483-65	US-09-820-002-2	US-09-000-846-2	US-09-820-002-4	US-09-079-970A-5	US-09-386-642-53	US-09-016-366A-19	US-08-978-404B-14	US-09-016-366A-21	US-08-978-404B-16	US-09-601-318-4	US-09-601-318-5	US-09-601-318-6	US-09-601-318-7	US-09-079-970A-6	US-09-601-318-1	US-09-027-337-3
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274	235	376	416	417	249	306	273	273	274	274	244	244	244	244	245	245	256
25.2	25.1	25.1	25.1	25.1	25.0	24.9	24.9	24.9	24.8	24.8	24.7	24.7	24.7	24.7	24.7	24.7	24.5
491.5	491	490.5	490.5	490.5	487.5	487	485.5	485.5	484.5	484.5	482.5	482.5	482.5	482.5	482.5	482.5	479
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

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Sequence 7, Application US/09386653A
Patent No. 6458564
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Patent No. 6485957
                                                                                                                                                                                 Patricia
274 GVFTAVATYEAWIREQV 290
                     262 GVYTSVATYSPWIQARV 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 316
TYPE: PRT
TYANISM: Artificial Sequence
FRATURE:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 7
                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Andrade-Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Homo sapiens US-09-386-653A-7
                                                                                          RESULT 3
US-09-386-653A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 GPFNLTLQILPGMLCAGYPEGRRDICQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP 273
                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                               287 REQVMGSEPGPAFFTQPQKTQSD---CLHQTAFLDS-ARILLRPLSHISVGVSTGTKSLV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 VHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHR 166
                                                                                                                                                                                                                                FVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLXSQPGPFNLTLQILPGM 226
                                                                                                                                                                                                                                                                                                      LCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWI 286
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                                                                                                                               47 IVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLG 106
                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 VCLPRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLX----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 CGQPRMSSRIVGGRDGRDGEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRAL---
                                                                                                                                                        1 ITGGSSAVAGQWPWQVSITYEGVHVCGGSLVSEQWVLSAAHCFPSEHHKE---AYEVKLG
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                                                        30.8%; Score 602; DB 3; Length 299; 41.4%; Pred. No. 2.4e-47; rive 48; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORRATION:
GENERAL INCORRATION:
APPLICANT: DATTOW, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Q1, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease BOS
TITLE OF INVENTION: Protease BOS
TITLE OF INVENTION: Protease BOS
TITLE OF INVENTION PROFES: 087,375
CURRENT PILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09387375 Patent No. 6485957
       No. 6232456e
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Best Local Similarity 46.3'
Matches 119; Conservative
                                                                               Best Local Similarity 41.49
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-09-387-375-7
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       MOLECULE TYPE:
             ; MOLECULE TYI
US-08-944-483-66
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US-09-387-375-7
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210 YSQPGPFNLTLQILPG-MLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCG 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 RNTSETSL-YQVLLGARQLVQP--GPHAMYARVRQVESNPLYQGTASSADVALVELEAPV 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 ARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 SLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCL
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.8%; Score 563; DB 4; Length 290; Best Local Similarity 42.2%; Pred. No. 8.6e-44; Matches 117; Conservative 32; Mismatches 114; Indels
APPLICANT: Darrow, Andrew
APPLICANT: Oi. Jian-shen
TITLE OF INVENTION: DNA encoding the novel human serine
TITLE OF INVENTION: Drotease T
FILE REFERENCE: ORT-1032
CURRENT APPLICATION NUMBER: US/09/386,653A
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
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APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Protease BOS
FILE REFERENCE: ORT-1031
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE PETELING VET: 2.0
SEQ ID NO 9
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39.3%;
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Best Local Similarity
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US-09-386-629-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 RETCHCLYNIDAKPEEPHFVQEDMVCAGYVEGGKDACÓGDSGGPLSCPVEGLWYLTGIVS 255
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                                                                           'n
                                                                                                                                                                                                                                                                                                          168 RPPPGTPCRVTGWGSLRPGVPLPEWRPLQGVRVPLLDSRTCDGLYHVGADVPQAERI--- 224
                                                                                                                                                                                                                                                                                                                                                                222 ILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVAT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CGVPDYKDDDDAAALAAPFDDDDKÍVGGYALBAGOWPWQVSITYEGVHVCGGSLVSEQWV 78
                                                                                                                                         46 RIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLL 105
                                                                                                                                                                                                 106 GVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADIALIRLASPASLGPAVWPVCLPRASH 165
                                                                                                                                                                                                                                                                              166 REVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLY----SQPGPFNLTLQ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGPAFPTQPQKTQSD---CLHQTAF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 CGRP------EPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWV
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                                28.5%; Score 557; DB 4; Length 316; 45.8%; Pred. No. 3.5e-43; Live 27; Mismatches 98; Indels
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GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Oi, Jenson
TILLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DARTE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
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Matches 116; Conservative
                                                            Best Local Similarity 45.83
Matches 114; Conservative
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US-09-387-375-9
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Best Local
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TITLE OF INVENTION: Identification and Characterization of the complementary TITLE OF INVENTION: Identification and Characterization of the complementary TITLE OF INVENTION: DNA encoding the novel human serine protease C-E FILE REFERENCE: ORT-1030
CURRENT APPLICATION NUMBER: US/09/386,629
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 RFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 MYCAGYVEGGKDACQGDSGGPLSCPVEGLWYLTGIVSWGDACGARNRPGVYTLASSYASW 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 RIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 MLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAW
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28.2%; Score 550; DB 4; Length 328;
Best Local Similarity 41.2%; Pred. No. 1.6e-42;
Matches 113; Conservative 41; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 IREQVMGSEPGPAFPTQPQKTQSD---CLHQTAF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 IQSKV--TELQPRVVPQTQESQPDSNLCGSHLAF 319
GENERAL INFORMATION:

APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Advade-Gordon, Patricia
APPLICANT: Advade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: OFF.1028
CURRENT FILING DATE: 1999-08-31
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 328
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Patent No. 6426199
GENERAL INFORMATION:
APPLICANT: Darrow, Andrew L.
APPLICANT: Q1, Jenson
APPLICANT: APLAGE-Gordon, Patricia
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US-09-905-125A-263
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LENGTH: 317
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APPLICANT:
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                                                                                                                                                                                                                                      PLPLPWVLQEVELRLLGEATCQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD 242
                                                                                                67 GGGHICGGSLIAPSWVLSAAHCFWTWGTLEPAAEWSVLLGVHSQDGPLDGAHTRAVAAIV 126
                                                                                                                                                                                                                                                                    ----ITEDMLCAGYLEGERDACLGD 241
                                                                                                                       7 LGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH 66
                                                            10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPWIVSIQK 69
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PPLICANT: Wood, William, I.
ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                           SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
 12;
Mismatches 123; Indels
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APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
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Grimaldi, Christopher J.
   41;
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Kljavin, Ivar J.
Mather, Jennie P.
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Filvaroff, Ellen
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Stewart, Timothy I
Tumas, Daniel
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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   Conservative
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     114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 NGTHHCAGSLLTSRWVITAAHCKKDN--LNKPYLFSVLLGAWQLGNPGSRSOKVGVAWVE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 LGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWPNIVSIQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 PLPLPWVLQEVELRLLGEATCQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDTCQGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41; Mismatches 123;
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/2314
PRIOR FILING DATE: 1999-110-05
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-29
PRIOR PLILING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-04
PRIOR PLILING DATE: 1999-12-06
PRIOR PLILING DATE: 1999-12-20
PRIOR PLILING DATE: 1990-12-20
PRIOR REPLICATION NUMBER: PCT/US99/30919
PRIOR PLILING DATE: 2000-01-05
NUMBER: PCT/US00/00219
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Gerritsen, Mary E.
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Best Local Similarity 39.33
Matches 114; Conservative
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Sao, Wei-Qiang
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Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Homo Sapien
US-09-907-794A-263
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
        243 SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                         242 SGGPLMCQVDGAMILAGIISWGEGCAERNRPGVXISLSAHRSWVEKIVQG 291
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PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PRILING DATE: 1999-07-26
PRIOR PLILING DATE: 1999-07-28
PRIOR PLILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: UCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PLILING DATE: 1999-09-08
PRIOR PLILING DATE: 1999-09-13
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21690
PRIOR PLILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLILING DATE: 1999-09-15
PRIOR PLILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-11-09
PRIOR PLILING DATE: 1999-11-09
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DR APPLICATION NUMBER: PCT/US99/23089

R FILING DATE: 1999-10-05

DR APPLICATION NUMBER: PCT/US99/28214

DR FILING DATE: 1999-11-29

DR APPLICATION NUMBER: PCT/US99/28313

DR APPLICATION NUMBER: PCT/US99/28564

DR APPLICATION NUMBER: PCT/US99/28564

OR APPLICATION NUMBER: PCT/US99/28664

OR APPLICATION NUMBER: PCT/US99/28664
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APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/30911
                                                                                                                                                                                                      ; Sequence 263, Application US/09902775A; Patent No. 6686451
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Grimaldi, Christopher J.
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Filvaroff, Ellen
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Hillan, Kenneth,
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Mather, Jennie P.
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Ashkenazi, Avi
Botstein, David
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Gao, Wei-Qiang
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                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                          RESULT 10
US-09-902-775A-263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLPLPWVLQEVELRILGERICQCLY---SQPGPFNLTLQILPGMLCAGYPEGRRDICQGD 242
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                                                                                                                                                             APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
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39.3%; Pred. No. 5.4e-42;
tive 41; Mismatches 123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 00/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-26
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-09-09
PRIOR PELING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-03
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PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-02-22
APPLICATION NUMBER: US 60/143,048
                                                                                Roy, Margaret Ann
Stewart, Timothy A.
                                                  Paoni, Nicholas F.
Mather, Jennie P.
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Best Local Similarity 39.34
Matches 114; Conservative
                                                                                                             Stewart, Timo
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 423
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ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-905-125A-263
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189 LPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPL- 247
                               761 L--ILQKGEIRVINQTTCENLLPQ-----QITPRMMCVGFLSGGVDSCQGDSGGFLS 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 CGGSLIAPSWVLSAAHCFMTNG--TLEPAAEWSVLLGVHSQ-DGPLDGAHTRAVAAIVVP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      761 L--ILQXGEIRVINQTTCENLLPQ-----QITPRMMCVGFLSGGVDSCQGDSGGPLS 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   641 CGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDOSQRSAPGVQERRLKRIISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ANYSOVELGADLALLIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SARIVGGSNAQPGTWPWQVSLHH-GGGHI
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                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease;
TITLE OF INVENTION: Overexpressed in Carcinomas;
FITLE OF INVENTION: Overexpressed in Carcinomas;
FITLE REPRENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 2000-08-23
PRIOR PRICATION NUMBER: 09/421,213
PRIOR APPLICATION: NUMBER: 09/421,213
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-02-20
PRIOR FILING DATE: 1998-02-20
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GENERAL INFORMATION:
APPLICANT: O'BRIGH, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 09/421,213
09/027,337
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                                                                                                     248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
                                                                                                                               811 SVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKE 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 VCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIRE 288
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40.2%; Pred. No. 4.8e-41;
Live 39; Mismatches 95
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Patent No. 6649741
                                                                                                                                                                                                                                                                            Sequence 2, Application US/09644600
Patent No. 6451500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 40.2*
Matches 113; Conservative
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US-09-644-600-2
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US-09-654-600A-2
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US-09-644-600-2
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APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CGGSLIAPSWVLSAAHCFMTNG--TLEPAAEWSVLLGVHSQ-DGPLDGAHTRAVAAIVVP 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                        67 GGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVTLGVHSQDGPLDGAHTRAVAAIV 126
                                                                                                                                                                                                                                                                                                                                                          10 LGGGCLGTFTSLLLLLASTAILNAARIPVPPACGKPQQLNRVVGGBDSTDSEWPWIVSIQK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 PLPHPQTLQXLXVPIIDSEVCSHLYWRGAGGGP----ITEDMLCAGYLEGERDACLGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 IGPGQLGAVANSDSYSLYGLVPSGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMG 292
                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                             Length 317;
                                                                                                                                                                                                                        27.9%; Score 544; DB 4; Length 31.39.3%; Pred. No. 5.4e-42; tive 41; Mismatches 123; Indels
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-027-337-2; Sequence 2, Application US/09027337B; Patent No. 5972616
                                                                                                                                                                                                                        Query Match 27.9
Best Local Similarity 39.3
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 27.6
Best Local Similarity 40.2
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 ARGPPYCGRPEP---
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ORGANISM: Homo sapiens
                                                                                                                       TYPE: PRT
CORGANISM: Homo Sapien
US-09-902-775A-263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5972616
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LENGIH: 855
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                                                                                                  LENGTH: 317
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrar
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
                                                                                                                                                                                                                           Query Match
Best Local Similarity 39.0
Matches 110; Conservative
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Eaton, Dan L.
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APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-907-794A-257
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
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                                                                                                                                                                                                                                              ---SARIVGGSNAQPGTWPWQVSLHH-GGGHI
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                34;
                                                                                                                                                                                 Length 855;
                                                                                                                                                                               27.6%; Score 540; DB 4; Length 85 40.2%; Pred. No. 4.8e-41; attive 39; Mismatches 95; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: HUMAN PROTEASE MOLECULES NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: «Unknown»
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Wohan-Peterson, Sheela
REGISTRATION NUMBER: 41,201
REFERENCE/DOCKET NUMBER: PF-0458 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
Hillman, Jannifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tow Y.
Shah, Purvi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
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CITY: Palo Alto
                                                                                                                                                                                                              39;
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                                                                                                                                                                                                                                                  32 ARGPPYCGRPEP----
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COMPUTER READABLE FORM:
PRIOR FILING DATE: 1999-10-20
                                                                                                                              ; OTHER INFORMATION: TADG-15
US-09-654-600A-2
                                                                                                                                                                                                                Matches 113; Conservative
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                                                                                TYPE: PRT
ORGANISM: Homo sapiens
               1998-02-20
NUMBER OF SEQ ID NOS:
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US-09-008-271A-3
                                             SEQ ID NO 2
LENGTH: 855
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Best Local
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84 FETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNIYLSPRY----LGNSPYDIA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 FMTNGTLEPAAEWSVLLG-VHSQDG--PLDGAHTR-AVAAIVVPANYSQVELG---ADLA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 LIRLASPASLGPAVWPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLL 201
                                                                                                                                                                                                                                                                                                                                                                                                                               83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 GEATCOCLYSOPGPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGIT
                                                                                                                                                                                                                                                                                                                                                                                    29 SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                Length 314;
                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3;
                                                                                                                                                                                                                                                                                                27.4%; Score 534.5; DB 3;
39.0%; Pred. No. 4e-41;
iive 53; Mismatches 100;
                                                                                                                                                                                                              CLONE: 789927
SEQUENCE DESCRIPTION: SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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             TELEPAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 314 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
TELEPHONE: 650-855-0555
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gao, Wei-Qiang
Gerber, Hanspeter
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and Transmembrane Polypeptides and Nucleic

CURRENT FILING DATE: 2001-07-17

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142 LIRLASPASLGPAVMPVCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRIL 201
140 LVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALPSPHTLQEVQVAII 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 NNSWCNHIFIK---YSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNGLWYQIGVV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 FMTNGTLEPAAEWSVLLG-VHSQDG--PLDGAHTR-AVAAIVVPANYSQVELG---ADLA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 SGPARGPPYCGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.4%; Score 534.5; DB 4; Length 314;
Best Local Similarity 39.0%; Pred. No. 4e-41;
Matches 110; Conservative 53; Mismatches 100; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 314;
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PRIOR PEDLICATION NUMBER: PCT/USO/04414
PRIOR PELLING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILLING DATE: 1999-07-07
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-26
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-28
PRIOR PELLING DATE: 1999-07-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-13
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-09-15
PRIOR PELLING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-29
PRIOR PELLING DATE: 1999-11-20
PRIOR PELLING DATE: 1999-12-20
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Job time : 46 secs
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CORGANISM: Homo Sapien
US-09-907-794A-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.
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us-10-037-417-46.rapb

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February 25, 2004, 15:49:38; Search time 641 Seconds (without alignments) 117.600 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                               US-10-037-417-46
1953
1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT NRW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBGOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                          Run on:
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ALIGNMENTS

	Description	Sequence 111, App	Sequence 2, Appli	Sequence 86, Appl	Sequence 262, App	Sequence 125, App	Sequence 2, Appli	Sequence 86, Appl	Sequence 87, Appl	Sequence 26, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 89, Appl	Sequence 8, Appli	
	ΩĨ	US-09-888-615-111	US-09-948-094-2	US-10-176-847-86	US-10-097-340-262	US-10-074-566-125	US-10-109-616-2	US-10-051-874-86	US-10-051-874-87	US-10-051-874-26	US-10-041-400A-7	US-10-041-264A-7	US-10-042-091A-7	US-10-051-874-89	US-10-311-035-8	
		1	0	14	14	15	14	15	15	15	13	13	13	15	16	
	Query Match Length DB	818	343	343	343	343	339	342	342	280	284	284	284	285	346	
æ	Query Match	77.1	35.3	35.3	35.3	35.3	32.1	31.8	31.7	30.2	30.2	30.2	30.2	29.9	29.8	
	Score	1505	069	069	069	069	627.5	621	620	590	290	290	590	583.5	582.5	
	Result No.	Т	7	m	4	Ŋ	9	7	80	9	10	11	12	13	14	

Sequence 219, App Sequence 1294, App Sequence 7, Appli Sequence 222, App Sequence 222, App	
US-10-074-978A-219 US-09-813-245-1294 US-10-041-066A-7 US-10-041-066A-7 US-10-028-072-222 US-10-123-904-222 US-10-123-904-222 US-10-140-470-222 US-10-176-921-222 US-10-176-921-222 US-10-176-921-222 US-10-176-921-222 US-10-176-91-222 US-10-142-431-222 US-10-142-431-222 US-10-142-431-222 US-10-142-431-222 US-10-142-431-222 US-10-142-431-222 US-10-143-142-222 US-10-143-142-222 US-10-143-322-222 US-10-143-322-222 US-10-123-108-222 US-10-123-108-222 US-10-123-232-222 US-10-123-232-222 US-10-123-232-222 US-10-123-232-222 US-10-123-232-222 US-10-13-23-222 US-10-13-23-222 US-10-13-328-222 US-10-13-328-222 US-10-13-328-222 US-10-13-328-222 US-10-13-328-222 US-10-13-328-222	
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RESULT II.

US-09-888-615-111

Sequence 111, Application US/0988615

Patent No. US2020064856A1

GENERAL INFORMATION:

APPLICANT: BLOWNAN, GREGORY

APPLICANT: CANNEEL, SEAN

APPLICANT: CHARYDCZAK, GLEN

APPLICANT: SUDARAMA, SUCHA

TITLE OF INVENTION: NOVEL PROTEASES

FILE REFERENCE: 036602/1214

FILE REFERENCE: 036602/1214

PRIOR PILLING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 150

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO 111

LENGTH: 818

TYPE: PRT

TYPE: PRT

GGGANISM: HOMO sapiens

US-09-888-615-111

Query Match 77.1%; Score 1505; DB 9; Length 818; Best Local Similarity 100.0%; Pred. No. 6.1e-122; Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2.2	1.	157	157
38 CGRPEPSARIVGGSNAQPCTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNCTLEP 97	38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWINGTLEP 97	98 AAEWSVLIGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157	98 AAEWSVLLGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
38	38	98	98
ζŏ	gg	δý	Db

158 VCLPRASHRFVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFN 217

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55

Gaps

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TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030 CURRENT APPLICATION NUMBER: US/10/097,340 CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 RDICOGDSGGPLVCEBGGRWFQAGITSFGFGCGRRNRPGVFTAVATYBAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                      TGWGDVQBADPLPLPWVLQBVELRLLGBATCQCLYSQPGPFNLTLQILPGWLCAGYPBGR 235
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                                                                                                                                                                                                                                    1 MAQKGVLGPGQLGAVANSDSYSLY-GLVPSGP----ARGPPYCGRPEPSARIVGGSNAQP
                                                                                                                                                                                                                                                                           1. MAQKGVLGPGQLGAVA----ILLIYLGLLRSGTGABGAEAP--CG-VAPQAKITGGSSAVA
                                                                                                                                                                                                                                                                                                                56 GTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFWTNGTLEPAAEWSVLLGVHSQDGPLD
                                                                                                                                                             Length 343;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                    49; Mismatches 129;
                                                                                                                                                               35.3%; Score 690; DB 14; 43.6%; Pred. No. 1.1e-51;
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/312,132
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 262, Application US/10097340
Publication No. US20030087250A1
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                   Query Match
Best Local Similarity 43.6
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: John MONAHAN
APPLICANT: Manjula GANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peter VEIBY
                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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US-10-097-340-262
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APPLICANT:
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
TITLE OF INVENTION: AND OVARIAN CANCER
FILLE REFERENCE: MRI-039
CURRENT APPLICATION NUMBER: US/10/176,847
CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 RDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRFGVFTAVATYEAWIREQVMGSEP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 TGWGDVQEADPLPLPWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGWLCAGYPEGR 235
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                                                                                                 LTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFT 277
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              Sequence 2. Application US/09948094
Sequence 2. Application US/09948094
Patent No. US20020090625A1
GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
APPLICANT: Wong, Kamuel
APPLICANT: Wong, Kwong-kwok
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin
FILE REPERENCE: 81994/828423
CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT PILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 343;
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                                                                                                                                                           AVATYEAWIREQVMGSEPGPAFPTQPQKTQSD 309
                                                                                                                                                                                    49; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similaricy --- Matches 156; Conservative
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ORGANISM: Homo sapiens
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US~10-176-847-86
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US-09-948-094-2
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APPLICANT: Allen, Keith D.

TITLE OF INVENTION: TRANSGENIC MICE CONTAINING CHANNEL

TITLE OF INVENTION: ACTIVATING PROTEASE 1 (CAP1) GENE DISRUPTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
32.1%; Score 627.5; DB 14; Length 339;
Best Local Similarity 41.4%; Pred. No. 2.9e-46;
Matches 144; Conservative 48; Mismatches 139; Indels 17;
                                                                                                                                                                                                                                                        Length 343;
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                             35.3%; Score 690; DB 15;
43.6%; Pred. No. 1.1e-51;
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CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT FILING DATE: 2002-03-28
PRIOR PILING DATE: 2002-03-29
PRIOR FILING DATE: 2001-03-29
PRIOR FILING DATE: 2001-08-08
RUNBER OF SEC ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                      49; Mismatches
PRIOR APPLICATION NUMBER: 60/291,766
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/314,007
PRIOR FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10109616
Publication No. US20030167484A1
                                                                               NUMBER OF SEQ ID NOS: 132
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 125
LENGTH: 343
                                                                                                                                                                                                                                                                                                          Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-10-109-616-2
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Best Local Similarity
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                             TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                      US-10-074-566-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GAHTRAVAAIVVPANYSQVELGADIALIRLASPASLGPAVWPVCLPRASHRFVHGTACWA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 DAKVSTLKDITPHPSYLQEGSQGDIALLQLSRPITFSRYIRPICLPAANASFPNGLHCTV 170
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                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQKGVLGPGQLGAVA----ILLYLGLLRSGTGAEGAEAP--CG-VAPQARITGGSSAVA 53
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APPLICANT: Gorman, Linda
APPLICANT: Gorman, Linda
APPLICANT: Paddimir Y.
APPLICANT: Patturalidhara
APPLICANT: Patturalidhara
APPLICANT: Struck, Muralidhara
APPLICANT: Sprewsh G.
APPLICANTON NUMBER: US/10/074,566
CURRENT APPLICATION NUMBER: 09/619,252
PRIOR APPLICATION NUMBER: 09/619,252
PRIOR APPLICATION NUMBER: 60/144,722
PRIOR APPLICATION NUMBER: 60/144,722
PRIOR PRILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-11-29
PRIOR PRILING DATE: 1999-11-29
PRIOR PRILING DATE: 1001-03-19
PRIOR PRILING DATE: 10001-03-19
PRIOR PRILING DATE: 2001-04-02
PRIOR PRILING DATE: 2001-04-02
PRING PAPLICATION NUMBER: 60/280,898
PRIOR FILING DATE: 2001-04-02
                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                      Length 343;
                                                                                                                                                                                                                                                                                                                   49; Mismatches 129; Indels
                                                                                                                                                                                                                                                                        35.3%; Score 690; DB 14; 43.6%; Pred. No. 1.1e-51;
      PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
TERGTH: 343
TYPE: RRI
TYPE: RRI
CRGANISM: Homo sapiens
US-10-097-340-262
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FILING DATE: 2001-11-14
APPLICATION NUMBER: 60/288,062
FILING DATE: 2001-05-02
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                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 43.69
Matches 156; Conservative
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APPLICANT: Padigaru, Muralidhara
APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
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Boldog, Ferenc
Vernet, Corine AM
Li, Li
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Tchernev, Velizar T
Zerhusen, Bryan D
FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Rattus norvegicus US-10-051-874-86
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Best Local Similarity 40.8
Matches 144; Conservative
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US-10-051-874-87
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TITLE OF INVENTION: PROTEINS, POLYNUCLECTIDES ENCODING THEM AND METHODS OF
ITILE OF INVENTION: USING THE SAME
                                                                                                                                                                                                                  238 TCOGDSGGPLVCEEGGRWFOAGITSFGFGCGRRNRPGVFTAVATYEAWIREQVMGSEPGP 297
                                                       HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
 56 WPWQVSIIYDGMHVCGGSLVSNKWVVSAAHCFPREHSRE---AYEVKLGAHQLDSYSNDT 112
                                                                           113 VVHTVAQIITHSSYREEGSQGDIAFIRLSSPVTFSRXIRPICLPAANASFPNGLHCTVTG
                                                                                                                           WGDVQEADPLPLFWVLQEVELRLLGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRD
                                                                                                                                                   298 AFPTOPOKTOSD---CLHOTAFLDSAR-ILLRPLSHISVGVSTGTKSL 341
                                                                                                                                                                                                                                                                                        291 RVVPQTQESQPDGHLCNHHPVFSSAAAPKLIRPVLFIPLGLTLGLTS 338
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CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/325,306
PRIOR APPLICATION NUMBER: 60/325,587
PRIOR PILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/262,587
PRIOR PILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/272,409
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Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
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APPLICANT: Alsobrook II, John P
APPLICANT: Colman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Boldog, Ferenc
APPLICANT: Vernet, Corine AM
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Smithson, Glennda
Baumgartner, Jason C
Herrman, John L
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Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Parturajan, Meera
Shimkets, Richard A
Pena, Carol EA
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Zerhusen, Bryan D
Millet, Isabelle
Miller, Charles E
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Stone, David J
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Shenoy, Suresh G
Casman, Stacie J
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Ellerman, Karen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAQKGVI,GPGOLGAVANSDSYSLYGLVPS--GPARGPPYCGRP-EPSARIVGGSNAQPGT 57
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40.8%; Pred. No. 1.1e-45;
tive 50; Mismatches 139;
PRIOR FILING JAIR: YOUTS 2.2, 454
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PLING DATE: 2001-05-17
PRIOR PLING DATE: 2001-05-17
PRIOR PLING DATE: 2001-05-17
PRIOR PRIOR DATE: 2001-05-18
PRIOR PRING DATE: 2001-18
PRIOR PRING DATE: 2001-11
PRIOR PRING DATE: 2001-01-31
PRIOR PRING DATE: 2001-01-31
PRIOR APPLICATION NUMBER: 60/265,530
PRIOR PRING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTING DATE: 2001-01-16
NUMBER OF SEQ ID NOS: 269
SOFTWARE: PATENTING DATE: 2010-01-16
TYPE: PRI
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Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
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233 ACQGDSGGFLSCPIDGLWYLAGIVSWGDACGAPNRPGVYTLTSTYASWIHHHV--AELQP 290
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Shimkets, Richard A
Pena, Carol EA
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MacDougall, John R
Malyankar, Uriel M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 HTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWPVCLPRASHRFVHGTACWATG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 WGDVQEADPLPLPWYLQEVELRILGEATCQCLYSQPGPFNLTLQILPGMLCAGYPEGRRD 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 WGHVAPSVSLOTFRPLOQLEVPLISRETCSCLYNINAVPEEPHTIQQDMLCAGYVKGGKD 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAQKGVLGPGQLGAVANSDSYSLYGLVPS--GPARGPPYCGRP-EPSARIVGGSNAQPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BULGES, CATHERINE E TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDE; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDE; TITLE OF INVENTION: USING THE SAME TITLE OF INVENTION: USING THE SAME TITLE REPERENCE: 2102-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-18
PRIOR FILING DATE: 2001-01-18
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-03-18
PRIOR FILING DATE: 2001-01-31
                                                                                                                                                                                                                                Mezes, Peter D
Kekuda, Ramesh
Tampier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
                                                                                                                           Baumgartner, Jason C
Herrman, John L
Peyman, John A
                                                                            Lepley, Denise M
Smithson, Glennda
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Stone, David J
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Best Local Similarity 40.8
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Ellerman, Karen
                                                                                                                                                                                                             Linda
                                                                                                                                                                                                                                                                                                                                                                iu, Xiaohong
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LENGTH: 342
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POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
298 AFPTQPQXTQSD---CLHQTAF-LDSARILLRPLSHISVGVSTGTKSLVLPWL 346
                                 291 RAVPQTQESQPDGHLCNHHPVFNLAAAQKLSRPILFLFLFLSLTKGLFSL---WL 340
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FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 60/268,595
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-09-27
PRIOR FILING DATE: 2001-01-18
PRIOR PELICATION NUMBER: 60/22,409
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-03-16
PRIOR PELING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-18
PRIOR PELING DATE: 2001-01-31
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Gorman, Lillar

Mezes, Peter D

:: Kekuda, Ramesh

I: Taupier Jr, Raymond J

Tr. Gerlach, Valerie

Trase, William M
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APPLICANT: Ellerman, Karen
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Burgess, Catherine E
TITLE OF INVENTION: USING THE SAME
                                                                                                                                                                                          Sequence 26, Application US/10051874 Publication No. US20040005557A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tcherney, Velizar T
Zerhusen, Bryan D
Miller, Isabelle
Miller, Charles E
Lepley, Denise M
Smithson, Glennda
Baungartner, Jason C
Herrman, John A
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
Vernet, Corine AM
Li, Li
Shenoy, Suresh G
Casman, Stacie J
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APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Of John Servine
TITLE OF INVENTION: Drotease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/042,091A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR PILING DATE: 1999-08-31
NUMBER OF ESQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                         APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine
TITLE OF INVENTION: Procease EOS
                                                                                                                                                                                                                                                                                                                                              FILE REFRENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,264A
CURRENT FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US/09/387,375
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.0
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                                                                                                                                                                                    Sequence 7, Application US/10041264A Publication No. US20020142446A1 GENERAL INFORMATION:
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262 GVYTSVATYSPWIQARV 278
                                             274 GVFTAVATYEAWIREOV
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US-10-041-264A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 QAERI---VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWVLVGVVSWGKGCALPNRP 261
                                                                                                                                                                                                                                                                                                                  98 AAEWSVILGVHSQDGPLDGAHTRAVAAIVVPANYSQVELGADLALLRLASPASLGPAVWP 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CGQPRMSSRIVGGRDGENDEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRBAL---
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                                                                                                                                                                                                                                                                                                                                            158 VCLPRASHREVHGTACWATGWGDVQEADPLPLPWVLQEVELRLLGBATCQCLY----SQP
                                                                                                                                                                                                                                                                                                                                                                                                                           28 CGQPRMSSRIVGGRDGRDGEWFWQASIQHRGAHVCGGSLIAPQWVLTAAHCFPRRAL---
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                                                                                                                                                                                                Gaps
                                                                                                                                                                                                10;
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30.2%; Score 590; DB 13; Length 284;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99; Indels 1
                                                                                                                                                        Length 280;
                                                                                                                                                      30.2%; Score 590; DB 15; Length 280
46.3%; Pred. No. 4.2e-43;
Live 29; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Oi, Jenson
TITLE OF INVENTION: Protease EOS
TITLE OF INVENTION: Protease EOS
FILE REPERENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/10041400A Publication No. US20020110895A1
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262 GVYTSVATYSPWIQARV 278
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                                                                                                                                                              30.2%
Query Match
Best Local Similarity 46.3%
Matches 119; Conservative
NUMBER OF SEQ ID NOS: 269
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 26
LENGTH: 280
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                                                                                                  ; ORGANISM: Homo sapiens
US-10-051-874-26
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                                                                                 TYPE: PRT
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205 QAERI----VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWULVGVVSWGKGCALPNRP 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 CGQPRMSSRIVGGRDGRDGEWPWQASIQHPGAHVCGGSLIAPQWVLTAAHCFPRRAL---
205 QAERI---VLPGSLCAGYPQGHKDACQGDSGGPLTCLQSGSWVLVGVVSWGKGCALPNRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
30.2%; Score 590; DB 13; Length 284;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99; Indels 1
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                      214 GPFNLTLQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRP 273
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TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
                                                                                                                                                97
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                                                                                                                                                38 CGRPEPSARIVGGSNAQPGTWPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEP
                                                                                                                                                                   28 CGQPRMSSRIVGGRDGEWPWQASIQHPGAHVCGGSLIAPQWVITAAHCFPRRAL---
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                                                                                                                    Gaps
                                                                                                                    10;
                                                                                     Length 284;
                                                                                                                    Indels
                                                                                                                    99;
                                                                                     Query Match
30.2%; Score 590; DB 13;
Best Local Similarity 46.3%; Pred. No. 4.3e-43;
Matches 119; Conservative 29; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 89, Application US/10051874
Publication No. US20040005557A1
GENERAL INFORMATION:
APPLICANT: Padigaru, Muralidhara
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Mezes, Peter D
Kekuda, Ramesh
Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
Vernet, Corine AM
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Malyankar, Uriel M
Patturajan, Meera
Shimkets, Richard A
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Herrman, John L
Peyman, John A
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Shenoy, Suresh G
Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
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Zerhusen, Bryan D
Millet, Isabelle
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Lepley, Denise M
Smithson, Glennda
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Stone, David J
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                 LENGTH: 284
TYPE: PRT
CRGANISM: Homo sapiens
US-10-042-091A-7
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US-10-051-874-89
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    SEQ ID NO 7
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58 WPWQVSLHHGGGHICGGSLIAPSWVLSAAHCFMTNGTLEPAAEWSVLLGVHSQDGPLDGA 117
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29.9%; Score 583.5; DB 15; Length
Best Local Similarity 43.3%; Pred. No. 1.6e-42;
Matches 127; Conservative 39; Mismatches 116; Indels
               TILLE OF LINGWILLON: USING THE SAME
FILE REFERENCE: 21402-245
CURRENT APPLICATION NUMBER: US/10/051,874
CURRENT FILING DATE: 2000-09-25
PRIOR PEDLICATION NUMBER: 60/268,595
PRIOR PELLING DATE: 2001-02-14
PRIOR PELLING DATE: 2001-09-27
PRIOR PELLING DATE: 2001-09-27
PRIOR PELLING DATE: 2001-09-27
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-28
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/226,454
PRIOR PELLING DATE: 2001-01-18
PRIOR PELLING DATE: 2001-01-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-03-16
PRIOR PELLING DATE: 2001-05-17
PRIOR PELLING DATE: 2001-01-10
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-17
PRIOR PELLING DATE: 2001-01-16
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APPLICANT: YUE, Henry.
APPLICANT: ELLIOTT, Vicki
APPLICANT: GANDHT, Ameena R.
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: TRIBOLLEY, Catherine M.
APPLICANT: TRIBOLLEY, Catherine M.
APPLICANT: DELEGEANE, Angelo M.
USING THE SAME
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NGUYEN, Danniel B
LEE, Ernestine A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Mus musculus
US-10-051-874-89
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US-10-311-035-8
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220 LQILPGMLCAGYPEGRRDTCQGDSGGPLVCEEGGRWFQAGITSFGFGCGRRNRPGVFTAV 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 VHSQDGPLDGAHTRAVAAIVVPAN----YSQVELGADLALLRLASPASLGPAVWPVCLP 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 RASHREVHGTACWATGWG-DVQEADPL-PLPWVLQEVELRLLGEATCQCLYSQPGPFNLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 29.5%; Score 575.5; DB 14; Length 255; 43.7%; Pred. No. 6.8e-42;
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        FILE REFERENCE GT900 NUMBER: US/10/221,097
CURRENT PILING DATE: 2002-09-06
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 2000-03-06
PRIOR PILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 52
SOCTWARE: FRALESC for Windows Version 3.0
SEQ ID NO 36
LENGTH: 255
TYPE: PRI
ORGANISM: Homo sapiens
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Best Local Similarity 43.79
Matches 128; Conservative
REFERENCE:
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APPLICANT: KEANNEY, Liam
APPLICANT: KEANNEY, Liam
APPLICANT: KEANNEY, Liam
APPLICANT: KALLICK, Deborah A.
TITLE OF INVENTION: Proceases
FILE REFERENCE: PI-0123 PCT
CURRENT APPLICATION NUMBER: 0002-12-10
FRIOR APPLICATION NUMBER: 60/212,336; 60/213,955; 60/215,396; 60/216,821; 60/218,946
PRIOR FILING DATE: 2000-06-16; 2000-06-22; 2000-06-29; 2000-07-07; 2000-07-14
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; OTHER INFORMATION: Incyte ID No. US20040023243A1 2256251CD1
US-10-311-035-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.8%; Score 582.5; DB 16; Length 43.8%; Pred. No. 2.4e-42; tive 38; Mismatches 104; Indels
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Publication No. US20030144476A1
GENERAL INFORMATION:
APPLICANT: Agarwal, Pankaj
APPLICANT: Murdock, Paul R.
APPLICANT: Rixxi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Xiang, Zhaoying
TITLE OF INVENTION: NOVEL COMPOUNDS
    HAFALIA, April
KHAN, Farrah A.
CHAMLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
ARVIZU, Chandra S.
TANG, Y. Chandra S.
TANG, Y. Roderick T.
AZIMZAI, Yalda
                                                                                                                                                                                                 LU, Yan
RAMKUMAR, Jayalaximi
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Matches 133; Conservative
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                                                                                                                                                                                                                                                            REDDY, Roopa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PERL Program
SEQ ID NO 8
                                                                                                                                                                                                                                           XU, Yuming
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AC093175
AB017638
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BC024903
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AXO98215
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BC061800
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AX474697
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BC062334
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AC009088
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AX335777
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em_htgo_mus:*
           em_htg_inv:*
em_htg_other:
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em_htg_mam:*
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em_htg_hum:*
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Query
Match Length DB
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1102
2457
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                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Q=/Cqq12_1/USPTO_spool_p/US10037417/runat_24022004_101038_17447/app_query.fasta_1.519
-Q=/Cqq12_1/USPTO_spool_p/US10037417/runat_24022004_101038_17447/app_query.fasta_1.519
-DEV=fasta_pool_p/US10037417_casta_p2n.rge -NxNMATCH=0.1_LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=DIOSUM62 - ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=ext -HEAPSIZE=560 -MINIEN=0 -MAXIEN=200000000
-USER=US10037417_@CGN 1 1_4958_Grunat_24022004_101038_17447 -NCFU=6 -ICFU=3
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                                                                            February 25, 2004, 15:51:34; Search time 3779 Seconds (without alignments) 4094.592 Million cell updates/sec
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1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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AK075142 Homo sapi AX34294 Sequence BD125219 Primer fo BD126485 Primer fo AX342936 Sequence AC009088 Homo sapi AX335777 Sequence BC01462 Homo sapi AX335677 Sequence AX40567 Sequence AX40567 Sequence AX40567 Sequence AX40567 Sequence AX44697 Sequence AX44697 Sequence AX46567 Sequence AX46567 Sequence AX46567 Sequence AX46567 Sequence AX46567 Sequence AX084115 Sequence AX166529 Rattus no AX084115 Sequence

AX512287 Sequence AX512289 Sequence AX480096 Sequence AX480935 Sequence BD127529 Primer fo

SUMMARIES

ALIGNMENTS

AB038244 Mus muscu AF378085 Mus muscu AF188613 Mus muscu AF202076 Rattus no BC061800 Rattus no AC124461 Mus muscu AC093175 Mus muscu AB012638 Rattus no

AY335911 Mus muscu BC003851 Mus muscu

AY262280 Mus muscu BC024903 Mus muscu AX676264 Sequence

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AR256990 AF536382 BC062334

Sequence

Sequence Xenopus 1

AX823252 8 BC056000 N

AY266139 Mus muscu AX675581 Sequence AC117170 Rattus no

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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U., Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D. Proteins and nucleic acids encoding same

Patent: WO 02053742-A 45 11-JUL-2002;
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                              LeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyProPheAsnLeuThrLeu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                 Plowman,G., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.
Charydczak,G.
Novel proteases
Patent: WO 200860-A 52 03-JAN-2002;
Sugen, Inc. (US)
Location/Qualifiers
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CC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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JP 2002017375-A/2960
JP 2002017375-A/2960
JP 2002017375-A/2960
JP 2000253172
JOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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1 (bases 1 to 2810)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                              178 TrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGlu 197
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                                                 ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
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YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI,
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HELLX RESEARCH INSTITUTE
OS HOMO SADIENS (Human)
PN JP 2002017375-A/2960
PD 22-JAN-2002
PP 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SI PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAWA, KEIICHI NAGAI SHINCHI KOJIWA,
SHINKICHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD127529.1 GI:23222474
DP 2002017375-A/2960.
Homo sapiens (human)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0246389-A 31.3-UUN-2002;
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                                                 258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
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/noTe="Incyte ID No: 2751509CB1"
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Sequence 31 from Patent WO0246383.
AX480935
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/organism="Homo sapiens"
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AK075142 2810 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90661 fis, clone PLACE1005003, weakly similar to PROSTASIN PRECURSOR (EC 3.4.21.-).

DEFINITION

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Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Sugiyama,T., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kawai-Hio,Y., Saito,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.

NEDO human cDNA sequencing project
Unpublished
Direct Submission
S. Chases I to 2810)
S. Chases I to 2810)
S. Chases I to 2810)
S. Chases I to 2810
S. Chases I Institute (supported by Ministry of Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; CDNA full institute (supported by Ministry of Chapan Contains and clone selection: Helix Research Institute (supported by Ministry Contains and Conse selection: Helix Research Institute (supported by Ministry Contains Anna Conse Selection: Helix Research Institute (supported by Ministry Contains Anna Conse Selection: Helix Research Institute (supported by Ministry Contains Anna Conse Selection: Helix Research Institute (supported by Ministry Contains Anna Conse Selection: Helix Research Institute (supported by Ministry Contains Contains Anna Conse Selection: Helix Research Institute (supported by Ministry Contains Co
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IGGWTEGSWILVGRAAVQSSTELFAAIGPEBAMISQTVGEANLLPPSGSPHWPTGGSNLC
PPELAKASGSPHAVYFLLLILGIGS"
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/note="cloning vector: pME185FL3"
300. 2600
/note="unnamed protein product"
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Conservative:
Mismatches:
AK075142.1 GI:22761040
oligo capping; fis (full insert sequence)
Homo sapiens (human)
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Location/Qualifiers
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us-10-037-417-46.p2n.rg

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Koga,H.

Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA-2002;
HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN 2 2002017375-A/650
PD 22-JAN-2002
PP 70-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
PI 158HI,
PI ISHII,
PI ISHII,
PI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
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1 (Dases 1 to 670)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Ota,T., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Primer for synthesizing fi
BD125219
BD125219.1 GI:23220164
JP 2002017375-A/650.
Homo sapiens (human)
                             1.28e-44
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49.67%
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Best Local Similarity:
Query Match:
                     Alignment Scores:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                            oAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAl
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Regulation of human prostasin-like serine protease Patent: WO 0198467-A 1 27-DEC-2001;
Bayer Akriengesellschaft (DE)
Location/Qualifiers
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Seguence 1 from Patent WO0198467.
AX342934
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Query Match:
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Primer for synthesizing full-length cDNA and use thereof.
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PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
                                                                                     primer for synthesizing full-length cDNA and use thereof FH K Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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UP 2002017375-A/1916.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                  Homo sapiens (human)
JP 2002017375-A/1916
22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length CDNA and use thereof FH Key Location/Qualifiers
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                                                                  Ota.T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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PN JP 2002017375-A/1916
PD 22-JM-2002
PD 22-JM-2002
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHJ
PI SHII, YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, SHINICHI KOJIWA,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                              Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 1916 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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Mismatches:
Indels:

    .670
    /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Regulation of human prostasin-like serine protease
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
                                                                                                                                                                       linear
                               197 GluLeuArgLeuLeuGlyGlu-AlaThrCysGlnCysLeuTyr 210
                                                               623 GAGCTAAGGNTGCTGGGCGAAGGCAACTGGTCAATGTCTCTAC 665
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/mol_type="unassigned DNA"
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                                                                                                                                   RESULT 10
AX342936/c
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Finishing Completed at Stanford Human Genome Center and Los Alamos National Laborators:
National Laborators
National Laborators
Ouality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire NOTE: This insert is not the entire sequence is 233.4kb). It is clipped at the overlap with AC135050.
The number of bases overlapped is 2575.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 127769)

DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (03-APR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 127769)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 127769) DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission Submission DOE Joint Genome Institute, 2800 Mitchell Submitted (29-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Only Mar 29, 2003 this sequence version replaced gi:29029216.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Lo 127769)
DOB Coint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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    127769
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2 (bases 1 to 127769)
DOE Joint Genome Institute.
Direct Submission
                                                                       AC009088.9 GI:29366934
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716.50
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Best Local Similarity:
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FEATURES Location/Qualifiers 11796 .1796	Alignment Scores: 2.46-29 Length: 1796 Prach. No.: 697.00 Matches: 160 Score: 160 Score: 55.29% Conservative: 49 Best Local Similarity: 42.33% Indeps: 36 Ouery Match: 6 Gaps: 11	MetalaGinLysGlyvalleuGlyProGlyGlnLeuGlyAlaValAlaAsnSerAspSer	200 . 36 . 260 .		11 48 13	Oy 136 LeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaVal 155 Db 542 TCCCAGGCGACATTGCACTCCTCCAACTCAGCAGACCCATCATCTCTCCCGCTACATC 601 OY 156 TrpProValCySLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175 Db 602 CGGCCCATCGCCTGCAGCGAACGCCTCCTCCCCAACGGCTTCACTGCACTGCACTGCACTGCACTGCACTGCTC 661	17	Db 722 CTCGAGGTGCTCTGATCGTGAGGTGTAACTGCCTGTACACCAGGCCCAAG 781 Db 722 CTCGAGGTGCTCTGATCGTGGAGAGGTGAACTGCCTGTACACACCAGGCCCCAAG 781 Cy 216 PheAsnLeuUhrleuGln11eLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg 235 Cy 236 ArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrp 255 Cy 236 ArgAspThrCysGlnGlyAspSerGlyGlyProCleuValCysGluGluGlyGlyArgTrp 255 Cy 236 ArgAspThrCysGlnGlyAspSerGlyGlyProCleuValCysGluGluGlyGlyArgTrp 255 Cy 236 ArgAspThrCysGlnGlyAspSerGlyGlyProCleuValCysGluGluGluGlyGlyArgTrp 255 Cy 256 PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgAspArgAshArgProGlyVal 275 Cy 256 PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgAshArgAshArgProGlyVal 275 Cy 1ACCTGACGGGCATTGTGAGGGAGAGACCTGTGGGGCCCCAACAGGCCTGGTGTG 961 Cy 1ACCTGACGGCATTGTGAGGGAGAGACCTGTGGGGCCCCAACAGGCCTGGTGTG 961
Oy 78 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThr 09 7.8 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThr 09 32028 GCCCCTCCTGGGTCTCTCCGCTGCTCATGACGTGAGTATTCGCCTGGTC 00 91	319	91	31728 91 31668	Teccccogradagategaacecragaacccccccagacaacecracracracracracracracracracracracracrac	Qy 125 evalValProAlaAsnTyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLe 145 Db 31488 CGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTGGGGCCGACCTGGCCCTGGCGCCT 31429 Qy 145 uAlaSerProAlaSerLeuGlyBroAlaValTrpProValCysLeuProArgAlaSerHi 165 Db 31428 GGCCTCACCCGCCAGGCCTGGCGCCGCGCTGCTGCCCCGCGCCTCACA 31369	Oy 165 SARGPheValHisGlyThrAlaCySTrpAlaThrGlyArspValGlnGluAlaAs 185	Oy 197 -GluLeuArgLeuGly 202 -:::	AKOSGILSI AKOSGILSI LOCUS AKOSGILSI AKOSGILSI AKOSGILSI AKOSGILSI AKOSGILSI LOCUS LO

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56 GlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySer 75
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/db_xref="GI:12655207"
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/db_xref="LocusID:5652"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC001462 1800 bp mRNA linear PRI 04-OCT-2003
Homo sapiens protease, serine, 8 (prostasin), mRNA (cDNA clone
MGC:1133 IMAGE:3138532), complete cds.
                                                                                                                                                                                                                                                                                                                                                                     :::|||:::::
1136 CTGGGCCTGGCTCTGGGC-----CTCCTCCCCATGGCTCAGCGAGCACTGAGCT 1186
                                                                                                                                                                                                              1016 CAGCCTCGTGTGCCCCAAACCCAGGAGTCCCAGCACCAGAACACACTCTGTGGCAGC 1075
                                                                                ----ACAGAÁCTC 1015
                                                                                                                                                                                                                                                                                                                       313 GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer 331
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Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                    -CysLeuHis 312
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1800)
276 PheThralaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer------
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On Aug 19, 2003 this sequence version replaced gi:12655206.
Contact: MGC help desk
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                                                      296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp-
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Tissue Procurement: ATCC
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ITGGSSAVAGOWPMOVSITYEGVHÜCGGSLVSEÖNVISAAHCFPSEHHKEAVEVKÜGA
HQLDSYSEDAKVSTLKDIIPHPSYLQEGSGGJLALLOLSRETTSRYTYERYENTELEAANA
PENDILHCYTYGWGHYAPRSYSLLTPREKYLOLBEVPLISRETCNCLYIDAKPBEPHFVÜ
EDWYGAGYVEGGKDACCGISGEPLSCPVEGLIWYLTGIYSWGDACGARNR PGVYTLASS
YASWIQSKVTELQPRVVPQTQESQPDSNLCGSHLAFSSAPAGGLIRPILFIPHGLALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 4 Row: j Column: 3
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21536453.
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Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,K.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,K.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,K., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
TBurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,B.D.
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/note="Tryp_SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:smart00020"
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                                                                                                                                                                    TCCCAGGGCGACATTGCACTCCTCCACAGCAACCATCACCTTCTCCGCTACATC 625
                                                                                                                                                                                                   TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175
                                                                                                                                                                                                                  96 GluproAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAsp 115
                                                                                                            116 GlyalaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGlu 135
LeulleAlaProSerTrpValleuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu 95
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ctcgaggtgcctctgatcagtcgtgagacgtgtaactgcctgtacaacatcgacgccaag
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cctgaggagccgcactttgtccaagaggacatggrgctgctgctgtgtgggggggg
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                                                                                      --- GCCTATGAGGTCAAGCTGGGGCCCACCAAGTTCCTACTCCGAG
                                                                                                                            GlyProAlaPheProThrGlnProGlnLysThrGlnSerAgp-
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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature
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Conservative:
Mismatches:
Indels:
                                                      Patent: WO 0194629-A 6286 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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09-JAN-2002

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DNA

Sequence 6286 from Patent W00194629.

AX335777

LOCUS

AX335777.1 GI:18126496

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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296 GlyproAlaPheProThrGlnProGlnLysThrGlnSerAsp------CysLeuHis 312
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277 attctgctctatcttggaltactccggtcgggagagagagagagagagagagactccc
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AX336076 GI:18126795
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Patent: WO 0194629-A 6585 13-DEC-2001.
Avalon Pharmaceuticals (US)
Location/Qualifiers

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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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KM Human; NOVX; neurological disorder; Alzheimer's disease;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW Huntington's disease; Parkinson's disease; pain; behavioural disorder;
KW addiction; tuberous sclerosis; cancer; immune disease; myasthenia gravis; asthma, arthritis; diabetes;
KW thyroiditis; cardiovascular disease; hypertension; reproductive disorder;
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
KW pancreatitis; cirrhosis; glomerular endotheliosis; bacterial infection;
KW polycystic kidney disease; endocrine disorder; obesity; cardiomyopathy;
KW atherosclerosis; cell signal processing-related disorder;
KW metabolic pathway regulation disorder; cytostatic; neuroprotective;
KW metabolic pathway regulation disorder; cytostatic; neuroprotectivic;
KW antinflammatory; immunosuppressive; analysesic; antiatherosclerotic;
KW dermatological; antibacterial; antiathritic; hepatotropic; neurogenesis;
KW differentiation; procliferation; motility; haematopoiesis; wound healing;
KW anglogenesis; forensic biology; transgenic animal; drug screening;
KW gene therapy; NOV14a; prostatin precursor-like; chromosome 16; gene; ds.
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-DEJEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DEJEXT=7_-
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08-JAN-2001; 2001US-0272817P.
05-JUL-2001; 2001US-031817P.
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05-JUL-2001; 2001US-0318405P.
12-JUL-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318405P.
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(CURA-) CURAGEN CORP.

Kekuda R, Algobrook JP, Tchernev VT, Liu X, Spytek KA;
Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li L;
Gorman L, Edinger S, Sciore P, Ellerman K, Malyankar U;
Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
Padigaru M, Taupier RJ, Miller CE, Eisen A;

WPI; 2002-583619/62. P-PSDB; ABB09523.

Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, trating cancer, atherosclerosis, neurological, skin and autoimmune disorders.

Claim 9a; Page 142; 323pp; English.

The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (AB093092). NOVX proteins and nucleic acids encoding them (AB093092). NOVX proteins and nucleotides are useful in the treatment, diagnosis or prevention of NOVX cassociated disorders or in the manufacture of a medicament for treating associated disorders or in the manufacture of a medicament for treating cassociated disorders or in the manufacture of a medicament for treating cassociated with Sports of them of the 24 cassociated with Sports of them of the 24 cassociated with NOVX proteins including neurological disorders (e.g., Alzheimer's Huntington's and parkinson's diseases), call sports are associated with NOVX proteins including neurological castor, path, behavioural disorders, addiction, tuberous sclerosis, cancers of e.g., allargies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., phypertension), reproductive disorates, endometriosis, incontinence, psoriasis, scleroderma, alopedia, ulcers, pancreatitis, incontinence, psoriasis, scleroderma, alopedia, ulcers, pancreatitis, circuminence, psoriasis, scleroderma, alopedia, ulcers, pancreatitis, diabetes, controlers, polycytic kidney diseases, endometriosis, circuminence, psoriasis, scleroderma, alopedia, ulcers, pancreatitis, diabetes, collections and particularly cardiomyopathy, disorders, obesity, bacterial infections and particularly disorders of metabolic pathway regulation. NOVX nucleic acids and polypeptides may of metabolic pathway regulation. NOVX nucleic acids sequences can be used to identify a cell differentiation, of small molecular and part modulate or inhibit processes such can necessure of proliferation of small molecular or probes for forms, or an electivity of NoVX proteins and per dentifying and cloning NoVX homologues in other cell types of NoVX activity. The present sequence represents of prostering

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                                                                       919 AGAATCCTTTTGAGGCCCTTTGTCCCATATATCAGTAGGAGTCTCAACTGGGACCAAAAGC 1038
                                              321 ArgileleuleuArgProleuSerHisileServalGlyvalSerThrGlyThrLysSer 340
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Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM,
Gorman L, Bdinger S, Sciore P, Bllerman K, Malyankar U;
Rothenberg M, Stone D, Boldog F, Guo X, Shenoy S, Anderson D
Padigaru M, Taupier RJ, Miller CE, Eisen A;
                                                                                                                                      1039 CITGICCICCCTGGCICICCCACACICICCTGGGGCCTCTGGGGGGIIC 1089
                                                                                                           LeuValLeuProTrpLeuSerProHisSerLeuLeuGlyLeuTrpGlyPhe 357
                                                                                                                                                                                                                                                                                                                                      Human; NOVX; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                       Human prostatin precursor-like NOV14b DNA, SEQ ID NO:45.
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/product= "NOV14b"
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28-FEB-2001; 2001US-0272411P.
02-MAR-2001; 2001US-0272811P.
05-JUL-2001; 2001US-030331P.
12-JUL-2001; 2001US-0305060P.
                                                                                                                                                                                                               ABQ93902 standard; DNA; 1102 BP
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2001US-0318700P.
2002US-00037417.
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The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ9302). NOVX proteins and nucleic acids encoding them (ABQ93879-ABQ9302). NOVX proteins and nucleic acids encoding them (ABQ93879-ABQ9302). NOVX proteins are useful in the treatment, diagnosis or prevention of NOVX-nucleotides are useful in the manufacture of a medicament for treating associated disorders or in the manufacture of a medicament for treating such disorders, with specific applications described for each of the 24 NOVX proteins, based on their homology to known proteins. Various disorders (e.g., Albrañagre) and about their homology to known proteins. Various disorders (e.g., albrañagre) addiction, tuberous sclerosis, cancers (e.g., albrañagre) and autoimmune disorsess, myasthenia gravis, asthma, various forms of arthritis diabetes, thyroiditis, cardiovascular disorders (e.g., hypertension), reproductive disorders, endometriosis, cardiomyopathy, cincontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, cincontinence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, disorders, obesity, bacterial infections and particularly disorders atheroselerosis, cell signal processing-related disorders and disorders and cincontinence in section and are also useful as targets for the binds to a NOVX protein, and are also useful as targets for the comprision of small molecules that modulate or inhibit processes such incleic acid sequences can be used to identify a cell of sequences can be used to identify a cell of comprision of small molecules in other cell types. Cells of are useful as a source of primers or probes for forensic biology and for are useful as a source of primers or probes for forensic biology and comprising NOVX mucleic acids are useful and are useful der identifying and cloning NOVX homologues in other cell types. Cells comprising or which and are useful and evaluating and evaluating and contains and fo
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                       Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 TyrSerLeuTyrGlyLeuValProSerGlyProAlaArgGlyProProTyrCysGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other;
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                                                                                                                                                 Claim 9a; Page 143; 323pp; English.
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TrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluProAlaAlaGlu 100 259 IGGGICCICICCGCIGCICACTGITICATGACGAATGGGAACGTIGGAGCCCGCGGGCCGAG 318

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                                                                                       AlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpProValCysLeu
                                                                                                                                                                                 ValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGluLeuArgLeu
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             119 TGGTCGGTACTGCGCGCGCGCCCCGGGCCCCCTGGACGGCGCGCACACCGC
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                                             AlavalAlaAlaIlevalvalProAlaAsnTyrSerGlnValGluLeuGlyAl
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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are and the nucleic acids encoding them. The sequences of the invention are cancer in ungy, immune-related diseases and disorders (e.g. breast, colon, lumgy, immune-related diseases and disorders (e.g. restenosis and diseases at thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic cisorders (e.g. disorders, obesity), inflammatory disorders (e.g. disorders, pain, sexual dysfunction, mood disorders, attention disorders, neurological disorders, hypertension, psychotic disorders, neurological disorders (e.g. Alzehmer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also cuseful for treating viral infections caused by human immunodeficiency virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (e.g. sequences encoding for the novel human proceases of the invention

Sequence 2457 BP; 377 A; 851 C; 797 G; 432 T; 0 U; 0 Other;

Alignment Scores:

Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory

Claim 26; Fig 1SS-TT; 313pp; English.

disorders.

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Caenepeel

Sudarsanam S, Manning G,

Whyte D,

Charydczak G;

Plowman G,

(SUGE-) SUGEN INC

WPI; 2002-139913/18. P-PSDB; AAU82753.

26-JUN-2001; 2001WO-US020171 26-JUN-2000; 2000US-0214047P

03-JAN-2002

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Human; protease; cancer; immune-related disorder; cardiovascular disease; neuronal-associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; pain; mod disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection; ocular disease; cytostatic; gene; ds.
                                                                                                                   DNA encoding novel human protease #52.
                            BP
                           ABK31795 standard; DNA; 2457
                                                                                        23-APR-2002 (first entry)
                                                           ABK31795;
RESULT 3
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WO200200860-A2 Homo sapiens

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137
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                                                                                       38 CysGlyArgProGluProSerAlaArglleValGlyGlySerAsnAlaGlnProGlyThr
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21-DEC-2000; 2000US-0257803P.
05-JAN-2001; 2001US-0260110P.
19-JAN-2001; 2001US-026851P.
25-JAN-2001; 2001US-0264623P.
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Anticonvulsant; neuroprotective; nootropic; cytostatic; antipsoriatic;
Anticonvulsant; dermatological; antidabetic; antipskrinsonian;
Anticanaemic; antilnflammatory; antiulcer; antiparkinsonian;
Anticanaemic; antilnflammatory; antiulcer; antipartelic; isrudide;
Anticanaemic; antilnflammatory; anticonation; virucide;
Antiparcerial; fungicide; gastrointestinal; antidatraheic; laxative;
Antiparcerial; antilarteriosclerobic; phycoensive; vasotropic;
Antitumour; antirheumatic; immunosuppressive; antialregic; antithyroid;
Antitumour; antisheumatic; immunosuppressive; antialregic; antithyroid;
Antitumological; antidepressive; intialregic; antinfertility;
Antition; protozoacide; cranquiliser; vulnerary; keratolytic;
Antition; protozoacide; Crohm's disease; hypertension; autoimmune;
Antitionmatory; anemia; cell proliferative; developmental; epithelial;
Antitiammatory; anemia; cell proliferative; developmental; epithelial;
Antitiammatory; gene therapy; vaccine; disorder; prostasin; gene; ss.
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138 AlaAspIeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpPro 157
                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated Protein Modification and Maintenance (PRM) polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. anaemia), cell hypertension), autoimmune/inflammatory disorders (e.g. anaemia), cell proliferative disorders, developmental disorders (e.g. anaemia), cell reproductive disorders (e.g. Alzheimer's disease) (e.g. scabise), meurological disorders (e.g. Alzheimer's disease) vaccine for such diseases. They may also be used in the assessment of the experions compound on the expression of nucleic acid amino effects of exogenous compound on the expression of nucleic acid amino effects of exogenous compound on the expression of nucleic acid and amino and accompanies.
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Azimzai Y, Kallick DA, Baughn MR, Griffin JA, Swarnakar A; Walia NK, Hafalia AJA, Gandhi AR, Au-Young J, Elliott VS; r J, Thangavelu K, Lu Y, Warren BA, Lu DAM, Lee EA; ey CM, Arvizu C, Delegeane AM, Yao MG, Khan FA;
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                             yalCysLeuproArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
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T, Koqa
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Ots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 AlaPheProThrGlnProGlnLysThrGlnSerAsp 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCTTTCCCACCCAGCCCCAGAAGACCCAGTCAGAT 927
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11-JAN-2000; 2000JP-00118774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine procease and reagents and methods for regulating prostasin-like enzyme activity. Prostasin is a trypsin-like the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease is useful for immunodetection and for prostasin-like serine protease is useful for immunodetection and diagnosis of micro-metastases, autoimmune lesions and renal failure in chopys speciments, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of used to modulate enzyme activity in a disease, such as metastasis of cused to modulate enzyme activity in a disease, such as metastasis of pulmonary disease (CODE), atheroselevosis, neurodegenerative disease (COPE), atheroselevosis, neurodegenerative disease (CoPE), atheroselevosis, neurodegenerative disease (CoECT), atheroselevosis, neurodegenerative provides a cherapeutic target of decreasing human prostasin-like serine provides a ctivity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                            Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmue lesion; abterosclerosis; gene; canal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Grentzfeldt-dakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; ss.
 863 IGCIGIGGCIACCIAIGAGGCAIGGAIACGGGAGCAGGIGAIGGGIICAGAGCCIGGGCC 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /partial
/note= "No start or stop codons shown"
                                          oAlapheProThrGlnProGlnLysThrGlnSerAsp 309
                                                             TGCCTTTCCCACCCAGCCCCAGAAGACCCAGTCAGAT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product= "Prostasin-like enzyme"
                                                                                                                                                                                                                                                               Human prostasin-like serine protease cDNA #1
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20-MAR-2001; 2001US-0276909P.
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216 phehsnieuThrieuGlnileLeuProGlyMetieuCysAladlyTyrFroGludlyArg 235
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augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like berine protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #1 nucleotide sequence of the invention
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                                                                                                                                                                                             Sequence 537 BP; 92 A; 176 C; 197 G; 72 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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us-10-037-417-46.p2n.rng

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The invention relates to primers for synthesising full length CDNA clones. 830 CDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence methods. The sequence was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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                                                                                                            503 TGICTGCCTGCCCCGCGCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGGGCCACCGG
                                                                  177 yrrpGlyAspVal-GlnGluAlaAspProLeuProLeuProTrpValLeuGln-GluVal
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T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; full length cDNA; cDNA synthesis; oligo-capping; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA clone representative sequence, SEQ ID NO: 1916.
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                                                                                                                                                                                                                                                        Ishii S, I
                                                                                                                                                                                                       GlureuargLeuLeuGlyGlu-AlaThrCysGlnCysLeuTyr
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K, Kojima ƙ
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su A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence fiths 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROW format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322
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T, Koga
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a T, Nagai K, Kojima
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Novel human prostasin-like serine protease polypeptide and polynucleotide
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eAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPr
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human prostasin-like serine protease cDNA #2.
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20-MAR-2001; 2001US-0276909P.
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ID ABK13566 standard; cDNA; 456
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which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections. By Disclosure; Fig 3; 111pp; English.

This invention comprises the CDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating prostasin-like serine protease is useful for immunodetection and care protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and capanosis of micro-metastases, autoinmune lesions and renal failure in bloopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of used to modulate enzyme activity in a disease, such as metastasis of cused to modulate enzyme activity in a disease, such as metastasis of pulmonary disease (COPD), atherosclerosis, neurodegenerative disease (COPD), atherosclerosis, pagett of disease in mucleotide sequence may be useful to treat administ and antagonists of the mucleotide sequence may be useful to treat augment and inhibit the enzyme activity which may be useful to treat or particularly dental implants. Alexed levels of human prostasion of estention and inhibit the progression of bone implants of atherosclerosis. The nucleic acid sequence is also useful in diagnostic atherosclerosis. The nucleic acid sequence of mutations in nucleic acid sequences cof diseases related to the presence of mutations in nucleic acid sequence (CCCC) which encode the enzyme. The presence of enteriors of the invention so prostasin-like serine protease #2 nucleoride sequence of the invention sequen
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Alignment Scores: 3.56e-36 Length: 456
Pred. No.: 799.00 Matches: 147
Score: 799.00 Conservative: 1
Best Local Similarity: 97.37* Mismatches: 4
Query Match: 6 Gaps: 0
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US-10-037-417-46 (1-357) x ABK13566 (1-456)

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ογ	97	ProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGly 116
qq	456	ccceceacceactratratratratratratratratratratratratrat
ò	117	AlaHisThrArgAlaValAlaAlaIleValValValProAlaAsnTyrSerGlnValGluLeu 136
qo	396	GCGCACACCGCNGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAGCTG 337
ò	137	GlyalaaspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrp 156
1 Q	336	GECECCACCTGGCCCTGCTGGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGG 277
Š	157	ProvalCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThr 176
: A	276	
è	177	GlyrroGlyAspValGluGluAlaAspProleuProLeuProTrpValLeuGluGluVal 196
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Ор	216	GGCTGGGGAGACGTCCAGGAGGCAGATCTTGCCTCTCTGCGTGCTGCTGCTGCTGCTGCTGCTGCT
δλ	197	GluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyProPhe 216
qq	156	GAGCTAAGGCTGCTGGGGGGGGGGCCACCTGTCAATGTCTCTACAGCCAGC
ò	217	AsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArg 236
qq	96	

237 AspThrCysGlnGlyAspSerGlyGlyProLeuVal 248

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed can divinity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and also assess hadself represent novel human diagnostic and considered the constant when the constant 
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                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #4844.
36 GACACCTGCCAGGGTGACTCTGGGGGGGCCCCTGGTC 1
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                                                                                                                                                ВЪ
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23-AUG-2000; 2000US-00649167
                                                                                                                                                AAS69040 standard; cDNA; 597
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                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                 AAS69040;
                                                                                            RESULT 10
                                                                                                                         AAS69040
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Conservative: Mismatches: Indels:

2e-35 787.50 94.41% 93.17%

> Score: Percent Similarity: Best Local Similarity:

Query Match: DB:

Alignment Scores:

Gaps:

Length: Matches:

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                                                                                                                                                                                                                                                                                                     nProGlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrPr
                                                                             GCCCTGGACGGCGCGCACCCCCCCGCGCAGTGGCCGCCATCGTGGTGCCGGCCAACTACAG
                                                                                                                             183 CCCGCCGTGTGGCCTGTCTGCCTGCCCGCGCCTCACACCGCTTCGTGCACGGCACGGC
                                                                                                                                                                                                         aCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpVa
                                                                                                                                                                                                                       243 CTGCTGGGCCACCGGCTGGGGAGACGTCCAGAGGCAGATCCTCTCCCCTGGGT
                                                                                                                                                                                                                                                        lleuglnGluValGluLeuArgleuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGl
                                                                                                                                                                                                                                                                    303 GCTACAGGAAGTGGAGGCTAAGGCTGCTGGGGGAGGCCACCTGTCAATGTCTCTACAGCCA
                                                                                                                                                                                                                                                                                                                           363 geceggicerrenacerenererechaningeen againgterageingen generalegen agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the presence of breast cancer in an individual, involves using specific polynucleotide markers.
                                                                                                                                                           152 yproklavalrypprovalCysLeuProkrgAlaSerHisArgPhevalHisGlyThrAl
                   GlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyVal-HisSerGlnAspGl
                                112 yProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSe
                                                                                                             rGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human breast cancer / ovarian cancer related coding sequence #43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; gene; ds; cytostatic; breast cancer; ovarian cancer.
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US-10-037-417-46 (1-357) x AAS69040 (1-597)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUN-2001; 2001US-0300159P.
27-JUN-2001; 2001US-0301351P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUN-2002; 2002WO-US019773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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The invention comprises a method for assessing whether a patient is
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XX SQ Sequenc	nce 1733 BP;	311 A; 578 C;	500 G; 344 T; 0 1	U; 0 Other;
Alignment Scores: Pred. No.: Score: Percent Similarit: Best Local Simila Guery Match: DB:	Scores: milarity: Similarity: h:	5.65e-30 697.00 55.29% 42.33% 7	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1733 160 49 133 11
US-10-037-	417-46 (1-35	57) x ABT31936 (1	딘	
ζζ	1 MetAlaGl	InLysGlyValLeuGl	MetAlaGlnLysGlyValLeuGlyProGlyGlnLeuGlyAlaVa	yAlaValAlaAsnSerAspSer 20
Db	99 ATGGCCCA	AGAAGGGGTCCTGGG	gccreeccadcreece	dergregee146
δά	21 TyrSerLe	euTyrGlyLeuVa	GlyLeuValProSerGlyPro	ro 35
Db	147 ATTCTGCT	rcrarcrredarracr	ccggrcaddaacagga	ATTCTGCTCTATCTTGGATTACTCCGGTCAGGGACAGGAGGGGGGAGGAGGAGGTCCC 206
δλ	36 ProTyrCys	sGlyArg	oSerAlaArgileValGlyG	31ySerAsnAlaGlnPro 55
Db	207TG	- -	ccaadcacccatcaca	dereckáckaráckarcacc 257
ζζ	56 GlyThrTrpPro	rpProTrpGlnValSe	rLeuHisHisGlyGly	OTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlyGlySer 75
QQ	258 ĠĠrcagro	geccrisecassircas	CATCACCTATGAAGGC	GTCCATGTGTGTGGTGGCTCT 317
δy	96	laProSerTrpValle	uSerAlaAlaHisCys	LO E
qa	зів стсететс	CTGAGCAGTGGGTGCT	GTCAGCTGCTCACTGC	3.7
δλ	96 GluProAlaAla	rg.	alLeuLeuGlyValHis	11 d
qq	378 ĠÀА	Ö	CAAGCTGGGGGCCCAC	GCTAGACTCCTACTCCGAG 42
ΟŻ	116 GlyAlaHi	isThrArgAlaValAl	.aAlaIleValValProAl	13
qq	429 GACGCCA	AGGTCAGCACCCTGAA	GGACATCATCCCCCA (GACGÓCAAGGICAGCACCCIGAAGGACÁÍCAICCCCCACCCCAGGTAÓCICCAGGAGGGC 488
λõ	136 LeuGlyA	laaspLeualaLeuLe	suArgLeuAlaSerPro	Ď
QΩ	489 TCCCAGG	gcgacarrecacrecr	rccaactcagcagacc	ບ ຄ
δ	156 TrpProVe	alCysLeuProArgAl	LaSerHisArgPheVa	TrpprovalCysLeuproArgAlaSerHisArgPhevalHisGlyThrAlaCysTrpAla 175
qq	549 CGGCCCA	rcrectractrecade	caacecrecifice	caacddcrccacrdcacrcrc 608
δλ	176 ThrGlyT:	rpGlyAspValGlnG]	luAlaAspProLeuPro	ThrdlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu 195
qq	609 ACTGGCT	deedtcardideccc	cercagidadechece	gacgóccaaccacriccágcaa 668
à	196 ValGluL	euArgleuleuGlyG	luAlaThrCysGlnCy	ValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro 215
qq	669 CTCGAGG	FGCCTCTGATCAGTC	stgagacereraacre	ccreracarceaceccase 728
č	216 PheAsnL	euThrleuGln1leL	PheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAl	heAsnLeuThrLeuGln1leLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg 235
qq	729 CCTGAGG	BAGCCGCACTTTGTCC	aagagacatgggggg	recreecrarersaseses 788
λŏ	236 ArgAspT	ThrCysGlnGlyAspS	erGlyGlyProLeuVa	ľ.
QQ	789 AAGGACG	accreckadadreker	cresesecceacrere	84
λζ	256 PheGlnA	AlaGlyIleThrSerP	heGlyPheGlyCysGl	1
qq	849 TACCIGA	acggcarrergager	ggggargccreteg	kscccschachsscreams 908

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The present invention describes a method for assessing whether a patient is afflicted with ovarian cancer by comparing: (1) the expression of a marker (1) (see AAF98594 to AAF98730), in a patient sample; and (2) the mormal level of expression of (1) in a control non-ovarian cancer sample, where a significant difference between the level of expression in (a) and (b) is an indication that the patient is afflicted with ovarian cancer. It have expositions and kits from the present invention can be used for: (1) assessing and treating ovarian cancer; (2) making isolated for: (1) assessing and treating ovarian cancer; (2) making isolated assessment; and (3) inhibiting ovarian cancer in a patient. AAF988573 to AAF98593 represent human kinase marker primærs and probes which are used in the exemplification of the present invention
                                                                                                                                                                                                                       1133
                                                                                 331
                  -----CysLeuHis 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detection, assessment, prevention and therapy of ovarian cancer, comprises detecting changes in the expression of a variety of markers.
276 PherhralaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro
                                                                                                                          313 GlnThrAlaPheLeuAspSer---AlaArglleLeuLeuArgProLeuSerHislleSer
                                                                                                                                                                                                           1083 CTGGGCCTGGCTCTGGGC-----CTCCTCTCCCCATGGCTCAGCAGCTCAGCCT
                                                                                                                                                                                                                                                                                1134 GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACAGGAGCCTGGTCCTTC 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ovarian cancer; identification; detection; characterisation; kinase; marker; cytostatic; antisense gene therapy; ds.
                                                                                                                                                                                                                                                       ------ProHisSerLeuLeuGlyLeuTrpGlyPhe 357
                                                                                                                                                                                         332 ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer
                                                               296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp-
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human ovarian cancer cell expressed sequence 10798
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                                                                                                                                                                                                                                                                                                                                                          AAF98698 standard; DNA; 1796 BP.
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21-MAR-2000; 2000US-0191321P.
31-MAY-2000; 2000US-0208382P.
20-JUL-2000; 2000US-00208467.
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1016 CAGCTCGTGTGCTGCCCCAAACCCAGGGGTCCCAGCCGACACGCAACCTCTGTGGCAGC 1075
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; 2001US-0276026P.
; 2001US-0311732P.
; 2001US-0323580P.
; 2001US-0324967P.
; 2001US-0325102P.
; 2001US-0325102P.
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19-SEP-2001; 2
26-SEP-2001; 2
26-SEP-2001; 2
26-SEP-2001; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 GlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp------CysLeuKis 312
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Conservative:
Mismatches:
Indels:
Gaps:
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                        511 G; 359 T;
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                        327 A; 599
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                        Sequence 1796 BP;
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of
                                                                    1076 CACCTGGCCTTCAGCTCTGCCCAGGGCTTGCTGAGGCCCATCTTTCTGCTGCCT 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
     331
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GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer
                                                                                                                                                                                                                                                                                  GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACAAGGAGCCTGGTCCTTC 1240
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Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB;
Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                                                                                                                                                 ---ProHisSerLeuLeuGlyLeuTrpGlyPhe
                                                                                                                                                                                                             ValGlyValSerThrGlyThrLysSerLeuValLeuProTrpLeuSer-
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contributuse with patients having an enhanced risk of developing covarian cancer (e.g. patients having a familial history of ovarian cancer (e.g. patients having a familial history of ovarian cancer.) The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain cal sorders (e.g. cerebral ocdema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with covarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastrasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the concern at risk of developing ovarian cancer. The present mucleic acid sequence encodes one of the ovarian cancer markers described in the
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U; 0 Other; T; O Sequence 1834 BP; 309 A; 621 C; 526 G; 378

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TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175
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Matches:
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799 CTCGAGGTGCCTCTGATCAGTCGTGAGACGTGTAACTGCCTGTACAACATCGACGCCAAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                                                                                                                                                                                                                                            276 PheThralaValalaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro
                                                                                                                                                                                                                                                                              313 GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer
                                                                                         296 GlyproAlaPheProThrGlnProGlnLysThrGlnSerAsp------CysLeuHis
                                                                                                                                                                                                                                                                                                      1153 CACCTGGCCTTTCCGCCCAGCCCTGGCTTGCTGAGGCCCATCCTTTTCCTGCCT
                         PheasnLeuThrLeuGlnIleLeuProGlyMetLeuCysalaGlyTyrProGluGlyArg
                                                  236 ArgaspIhrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrp
                                                                                                                           256 PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVal
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(AVAL-) AVALON PHARM.

000US-0237606P.

000US-0237425P

Horrigan S; Endress G, Ebner R, Carter KC, Augustus M, Weaver Z;

WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 6286; 44pp; English

The present invention describes a method (MI) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity, and can be used in gene therapy. MI can be used for screening and activity and can be used for producing a product which is anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseoplageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, clear call cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's

Sequence 1834 BP; 309 A; 621 C; 526 G; 378 T; 0 U; 0 Other;

Length:
Matches:
Conservative:
Mismatches:
Indels: 5.97e-30 697.00 55.29% 42.33% 35.69% Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-037-417-46 (1-357) x ABL67949 (1-1834)

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δλ	36 Pr	<pre>IyrCysGlyArgProGluProSerAlaArg1leValGlyGlySerAsnAlaGlnPro 55 </pre>
Db	337	TGCGGTGTGGCCCCCCAAGCACGCATCACAGGTGGCAGTGCAGT
λö		S .
Dp	388 9	4,
8 8	u d	LeulleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu 95
gg	20	GAGGAGTGCTGTCAGTGCTTCACTGCTTCCCAGCGGGGCGCGCGGGGGGGG
දු දු	96 GI	GlubroAlaAlaGlubrpSerValLeuleuGlyValHisserGinAspGifyFroLeuksp 115
à		GlyAlaHisThrArgAlaValAlaAlaileValValProAlaAsniyrSerGlnValGlu 135
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δδ	236 A	ArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGluGlyGlyArgTrp 255
qu	919 A	iii agaacgeerigeeaagargaetereegaggeeeaachereeaagagaetereega 978
č	256 P	PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVal 275
Ωp	979 T	:: accreacescarrereageregeagareccreredegecceechacaegeccreerere 1038
ò	276 P	295
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Qy	296 G	GlyproAlaPheProThrGlnProGlnLysThrGlnSerAspCysLeuHis 312
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qq	1264 G	SECCETACTICCAGGAIGGAIGCAICACACICAAGGACAGGAGCCIGGICCIIC 1317

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent neoplastic activity, determining a change in cypression of at least one gene (1) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises a sequence (S) selected from 8447 sequences (given in ABL61664 comprises in indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an activity and can be used for producing a product which is anti-neoplastic agent, and can be used for producing a product which is compreted with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oseophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell carcinoma, neuroendocrine carcinoma, papillary carcer, squamous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAsp 115
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25-SEP-2000; 2000US-023503P.
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Weaver Z;
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                                                                                                                               15-MAY-2002
                                                                                            ABL68512;
                                                                                                                                                                                                            Human:
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              RESULT 15
                                ABL68512
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155

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1263
                                                                                                                                                                                                            313 GlnThrAlaPheLeuAspSer---AlaArgIleLeuLeuArgProLeuSerHisIleSer 331
                                                                                                                                                                                                                                                                   276 PherhralaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluPro 295
                                                                                                                                                                                                  296 GlyproAlaPheProThrGlnProGlnLysThrGlnSerAsp------CysLeuHis 312
                                                                         256 PheGlnAlaGlylleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVal 275
                                                           216 PheAsnLeuThrLeuGln1leLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg 235
196 ValGluLeuArgleuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro 215
                                     1264 GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACAGGAGCCTGGTCCTTC 1317
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Search completed: February 25, 2004, 16:16:14 Job time : 429 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

February 25, 2004, 15:57:04; Search time 2489 Seconds (without alignments) 4283.165 Million cell updates/sec 1 MAQKGVLGPGQLGAVANSDS......TKSLVLPWLSPHSLLGLWGF 357 US-10-037-417-46 1953 Title: Perfect score: Sequence: Run on:

0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table:

27513289 segs, 14931090276 residues Searched:

55026578 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
-MODEL=frame+ pAn.model -DEV=xlp
-MODEL=frame+ pAn.model -DEV=xlp
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-Ge/cgn2_1/USPTO_spool p/US10037417/runat_24022004_101038_17460/app_query.fasta_1.519
-DECALIGN=200 -TRN SCORE=pct -TRN MAX_100 -TRN WINS=0 -ALIGN=15. -MODE=LOCAL
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=0 -TRANS=human40.cdi -LIST=45
-UNITS=bits -TRNE=1 -END=-1 -MAX_100 -TRN WINS=0 -ALIGN=15 -MODE=LOCAL
-UNITSHT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=USI0037417_@CGN 1 1 3549_@runat_24022004_101038_17460 -NCPU=6 -ICPU=3
-NO MANP -LARGEQUERY -NEG SCORES=0 -MAX_T -DSPBALCOK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELDEXT=7

EST:*

Database

em_gss_vrt:*
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em_gss_mam:* em gss mus:* em_gas_hum:* em_gss_inv:* em_gss_pln:* 1: em_estba:*
2: em_estbum:*
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7: em_estpl:*
9: gb_est1:*
10: gb_htc:* em_gss_pro:* em_estfun:* em_estom:* gb_est4:* gb_est5:* gb_est3:* 18: 19:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

UI-H-BI3-akn-g-11-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens CDNA clone IMAGE:2735037 3', mRNA sequence. AW450407.1 GI:6991183 EST. RESULT 1 AW450407/c LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Homo sapiens (human)
Homo sapiens
Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini, Hominidae, Homo.
1 (Bases 1 to 537) REFERENCE

em_gss_rod:*
em_gss_phg:*
em_gss_vrl:*
gb_gssl:*

AUTHORS JOURNAL

COMMENT

FEATURES

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AI190509
AI190509.1 GI:3741718
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Homo sapiens
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                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Oligo-dr track not found, Not I site shown in beginning of sequence
oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Seg primer: M13 Forward
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2735037"
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TAG_SEQ=AAACG"
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ORIGIN

Score:

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AI190509 456 bp mRNA linear EST 28-OCT-1998 qd49f07.xI Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1732837 3' similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE 6 PRECURSOR; , mRNA sequence.
                       417
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seg primer: -400P from dibco
High quality sequence stop: 452.
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 ValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyPro
416 GGGGGCGCACCCGGGCAGTGCCGCCATCGTGGTGCCGGCCAACTACAGCCAAGTGGAG
                                                                                                                                                           LeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaVal
                                                                                                                                                                                   356 CTGGGCGCCGACCTGGCCCTGCCGCCTGACCTCACCGCCAGCCTGGGCCCGGC
                                                                                                                                                                                                                                                        156 TrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla
                                                                                                                                                                                                                                                                              296 TGGCCTGCCTGCCTGCCCCGCGCCTCACACCGCTTCGTGCACGCGCACCGCCTGCTGGCC
                                                                  GlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol type="mRNA"
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/clone="IMAGE:1732837"
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Score:

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Group Phase I E II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

E 6 (bases 1 to 1659)

S Adachi,J., Aizawa,K., Akimura,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Fukuda,S., Furuno,M., Hiramoto,K., Hiracka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Kondo,S., Konno,H., Kawai,J., Kojina,Y., Kondo,S., Konno,H., Kouda,M., Kaya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamira,M., Nishi,K., Nomura,K., Ninazaki,R., Sakai,K., Takaku-Akahira,S., Takada,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Phiracki,Y., Phiracki,Y., Tomaru,A., Toya,T., Yasunishi,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (16-ARR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunco,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Imoue,K., Togawa,Y., Izawa,M., Ohara,B., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Yokazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system—384-format sequencing pipeline with 384 multicapillary sequencer
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evidence: FASTY, 98.5%ID, 100%length, match=1020)
putative"
/codon_start=1
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Nature 409, 685-690 (2001)
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URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGly 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 CCTGTCTGCCTGCCCGCGCCTCACACCGCTTCGTGCACGGCACCGCCTGCTGGGCACC 217
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
(Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NDHL19W."
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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Mus musculus (house mouse)
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Best Local Similarity:
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AK010640 1629 bp mRNA linear HTC 20-SEP-2003 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410039E18 product:PROSTASIN, full insert sequence.
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Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPhe :
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                                                                                               GlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPhe
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Idjh-efficiency full-length cDNA cloning
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                      /db_xref="G1:26347427"
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QQDMLCAGYVKGGKDACQGDSGGPLSCPMEGIWYLAGIVSWGDACGAPNRPGVYTLTS
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                                                            21 TyrSerLeuTyrGlyLeuValProSerGly---ProAlaArgGly---ProProTyrCys
                                                                                                                                                                                             TrprotrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIle
                                                                                                                                                                                                                                                                                   78 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPro
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TCAAATAAATGGGTGGTGTCTGCTGCTCCCTGCTTCCCCAGAGAACACAGGGAA---
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                                                                                             CIGCICCTICICGGATIGCICCAGICGGGAAICCGAGCTGACGGGACTGAAGCCICCTGI
                                                                                                                                                            GlyArgPro---GluProSerAlaArgileValGlyGlySerAsnAlaGlnProGlyThr
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                 115 ATGGCCCTAAGGGTGGGCCTGGACTTGGGCAGCTGGAAGCTGTGACC---
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Mature 420, 563-573 (2002)

S Adachi, J. Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakwa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayateu, N., Hiramoto, K., Hiraoka, T., Hori, F., Inchani, K., Ishii, Y., Toh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nimazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Shibata, Y., Shibata,
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Clone_lib="RIKEN full-length enriched mouse cDNA library"
115. .882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="unnamed protein product; PROSTASIN (SPTR|BAB82496, evidence: FASTY, 98.5% of 100% length, match=1020)
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Conservative:
Mismatches:
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/db_xref="MGI:19<u>1</u>0128"
/db_xref="taxon:10090"
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'db_xref="G1:26370154"
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/strain="C57BL/6J"
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Best Local Similarity:
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RZPDLIB.
No.998) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
lin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
laevis Unidene Set I (RZPDLIB No.988) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 101
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                                                                                                                                                                                                                                                                                                                                                                 156 TrpprovalCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAla 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 GlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGlu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: SP6, 5' ATTAGGTGACACTATAG 3'.
                                                                                                                                                                                                                                                     538 TCCCAGGGGGACATTGCACTCCTCCTCCAACTCAGCAGACCCATCACCTTCTCCCGCTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 ThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         478 GACGCCAAGGTCAGCACCCTGAAGGACATCATCCCCCCACCCCCAGCTACCTCCAGGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                           598 CGGCCCATCTGCCTCCCTGCAGCCAACGCCTCCTTCCCCAACGGCCTCCACTGCACTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717 CTCGAGGTGCCTCTGATCAGTCGTGAGAGTYGTAACTGCCTGTACAACATCGACGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 PheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 ArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 PheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyVal
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                                                                                                                                                                                                       136 LeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaVal
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1 (bases 1 to 911)

2 (bases 1 to 911)

2 (bases 1 to 911)

3 (bases 1 to 911)

4 (and published (2003)

5 (bases 1 to 801)

6 (bases 1 to 801)

6 (bases 1 to 801)

7 (bases 1 to 801)

8 (bases 1 to 801)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 TACACTCTGGCCTCCAGCTATGCCTCCTGGATC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1071)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7896.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgi-bin/cluster.cgi?seq=CSOD1064DC010Pl&cluster=7896.r. Contact Feng Liang Email: fliangalifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSOD1064DC010Pl.
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                                                                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced
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                                         clone CS0DI064YF02 5-PRIME, mRNA sequence.
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AL551470.2 GI:31273286
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Mus musculus 3 days neonate thymus CDNA, RIKEN full-length enriched library, clone:A630023F11 product:similar to MARAPSIN FRECURSOR (EC 3.4.21.-) [Homo sapiens], full insert sequence.
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Nature 420, 563-573 (2002)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyo,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group Phase I'& II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                       SerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThrAlaValAlaThr 281
                                                                                                               242 AspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThr 261
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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                                              734 GACTCTGGAGGACCTCTTGTATGCAGAGTCAACAACACATGGTGGCAATACGGCATTGTC
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Gasterosteiformes;
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LEGEMPWQVSIQRNCIHFCGSSLIAFTWVLTAAHGFSNTSDISIYQVLLGALKLOQPG
PHALYVPKQKYKSNPQYQGMASSADVALVELQGPVFTNYILPVCLEDPSVIFESGNN
WYGWGSPSEQDRLPNPRUQKLAVPIIDTEKCNLLYNKDVESDFQLKTIKDDMLCA
GFAEGKKDACKGDSGGPLVCLVDQSWVQAGYISWGEGCARRNRFGYXIRVTSHHKWIH
QIIPPLQFQGGRAGTQQQQKDSQGQRLAGNSAPCLAAHAWILALGALLLRIV"
                                                                                 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9216,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |db_xref="FANTOM DB:A630023F11"
|db_xref="MGI:2406613"
|db_xref="taxon:10090"
|clone="A630022F11"
|tissue type="thymus"
|clone_lib="RIKEN full-length enriched mouse cDNA library"
|dev stage="3 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="unnamed protein product; putative similar to MARAPSIN PRECURSOR (EC 3.4.21.-) [Homo sapiens] (SWISSPROT|Q9EQR3, evidence: FASTX, 76.5%ID, 100%length,
                                                                                                                                                                                                                                          EDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.
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      Takahashi, F., Takaku-Akahira, S.
Toya, T., Yasunishi, A.,
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/db_xref="GI:2634849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
Sogabe,Y., Tagami,M., Tagawa,A.,
Takeda,Y., Tanaka,T., Tomaru,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
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E (lark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Bddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Washu Zebraish EST Project 1998

L Unpublished (1998)
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hab64c07,y1 Fugu UT7 adult skin Takifugu rubripes cDNA clone
IMAGS:6352269 5' similar to TR:09PVX7 09PVX7 EPIDERMIS SPECIFIC
SERINE PROTEASE. ;, mENA sequence.
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Email: abrafish@watson.wustl.edu
Library materials provided by G. Elgar (UK MRC HGMP-RC) Library
constructed by Drs. K. Kawakami, M. Sasaki, S. Sugano, K. Kikuchi
and S. Watabe (University of Tokyo, Institute of Medical Science
and Laboratory of Aquatic Molecular Biology and Biotechnology) DNA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                         Contact: Kingsley, DM
HHMI and Department of Developmental Biology
Stanford University School of Medicine
Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
                         1 (bases 1 to 1044)
Kingsley,D.M., Peichel,C., Balabahdra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
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tissue_type="heads and internal organs combined"
                                                                                                                 Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
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119
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Mismatches:
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/strain="Salinas river, CA"
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                                                                                                                                                                                                                                                                                        Tel: 650 725 5954
Fax: 650 725 7739
Email: kingsley@cmgm.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 793.
Location/Qualifiers
1. .1044
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Gasterosteidae; Gasterosteus.
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L (Dases I to 1189)

Altschuid, S.F., Reberg, B., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Colling, F.S., Wagner, L., Schaefer, C.F., Bhat, M.K., Altschuid, S.F., Zeeberg, B., Buet, M.K., Schaefer, C.F., Bhat, M.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, R.F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M. B., Bondloo, W.F., Casavanth, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Mallah, S.S., Louaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Sodrey, S.W., Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lux, C., Shevchenko, Y. Fahey, J., Helton, B., Kettemn, M., Madan, A., Young, A.C., Shevchenko, Y., Bukkelseley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Gohen, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse odna Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BC034294 1188 bp mRNA linear HTC 17-DEC-2003
Homo sapiens cDNA clone IMAGE:4752547, containing frame-shift
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Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1188)
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                                                                                                                                                                                                                                                                      238 ThrCygGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGln
                                                                                                                                                                                                                                                                                                                                           ---GTGGGAAGGATAACGGACAACATGGTCTGTGCCGGGTTGCGCAGCGAGGCAAAGAT
                                                                                             218 LeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAsp
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Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 AlavalAlaThrTyrGluAlaTrpileArgGluGlnVal 290
562 GIGCCCAICAGGGGAACAGGGAGIGIAACIGIAACIACGGA-
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Contact: MGC help desk
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Homo sapiens
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Strausberg, R.
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Seq primer: T3 ET from Amersham
High quality sequence stop: 490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98 AlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 AGCAGCGTG---ACCGTGTATCTGGGTCGTCAGAGCCAGGGGCTCCAACCCCAACGAG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 GAGGCGCTGAGAGTCACACAGATCATCATCATCCGGACTACAACTCGAATACGATTAAC 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 AlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpPro 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CysGlyArgProGluProSerAlaArgIleValGlyGlySerAsnAlaGlnProGlyThr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 TrpProTrpGlnValSerLeuHisHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyErLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPro
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                              /organism="Takifugu rubripes"
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/db_xref="taxon:31033"
/clone="IMAGE:6353269"
/esx="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-037-417-46 (1-357) x CA588481 (1-819)
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43.87%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                                                                                   FEATURES
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/tissue type="neurnla"
/dev stage="meurnla"
/dev stage="membryo, stages 14-19"
/lab_host="DH10B (phage-resistant)"
/clone lib="NH10B XGC Emb6"
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cloned unidirectionmally. Primer: Oligo dT. Average insert
size 2.1 kb. Constructed by Invitrogen. Note: This is a
Xenopus Gene Collection (XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 05-AUG-2003
                                                                                                                                                                   877
                             249 CysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGly 268
                                                                                                                                                                                                              277 -----ThralaValalaThrTyrGluAlaTrp11eArgGluGlnValMetGly 292
                                                                                                                                                                                                                                                                                                           293 SerGluProGlyProAlaPhePro------ThrGlnProGlnLySThrGln 307
                                                                                                                                                                                                                                                                                                                                                         Xenopodimae; Silurana, Annia, Resonariatina, ripotaca, ripitace, Senopodimae; Silurana, 1 (bases 1 to 938)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Betheada, MD 20992
Email: Gapbbs-remail.nih.gov
Tissue Procurement: Robert M. Grainger
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at:
http://image.lln.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silurana tropicalis (western clawed frog)
Silurana tropicalis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF238383
AGENCOURT_15097797 NICHD_XGC_Emb6 Silurana tropicalis cDNA clone
MACE:6993385 5', mRNA sequence.
                                                                                                                                                  758 TGCCTCGTGGGTCAGTCGTGGCTGCAGGCGGGGTGATCAGCTGGGGTGAGGGCTGTGCC
                                                                                                                                                                                                                                                          878 GATCATCCCCAAACTGCAGTTCCAGCCAGCGAGGTTGGG----CGGCCAGAAGTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                   986 ------càccarcracracracracracacacacrarr 1018
                                                                                                                                                                                                                                                                                                                                                                                                       308 SerAspCysLeuHisGlnThrAlaPheLeuAspSerAlaArgIle 322
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: LLAMI4673 row: 1 column: 24
High quality sequence stop: 724.
Location/Qualifiers
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                                                                                                                       269 ArgArgAsnArgProGlyValPhe--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF238383.1 GI:33441591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF238383
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                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 52 Row: d Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13994275
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 AsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAsp 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValProAlaAsn--- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgleuAlaSerProAla 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerLeuGlyProAlaValTrpProValCysLeuProArgAlaSerHisArgPheValHis 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyThrAlaCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeu 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCATGAACTGCTGGGTCACTGGCTGGGCAGCCCCAGTGAGGAAGACTCCTGCCCGAA 5777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AsnAlaGlnProGlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIle 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGly---MetLeuCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1188
128
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118
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                                                                                                                                                                                                                                                                                                                                                                                                   'note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                          1. .1188
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50.79%
40.63%
28.44%
A.N., Gibbs, R.A.
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Best Local Similarity:
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Pred. No.:
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/clone="tcba00080.j.09"
/tissue_type="multi-tissues"
/tesue_type="multi-tissues"
/dev_stage="from embryos to adults"
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                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::: |||::: |||::: |||242 TCTCAGATCATCATCATCATGATATATGTTTG
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                                                        Actinopterygii, Deopterygii; Teleostei, Euteleostei; Euteleostei; Protacanthopterygii, Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 777)
Govoroum,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                   chromatogram of
                                                                                                                                                                                                                                                                                                                                                             Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions.
at sigenasupport@jouy.inra.fr to obtain the chromatogra
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                                                                                                                                                                                                                                          Contact: Guiguen Y
Contact: Guiguen Y
INRA - SCRIBE
Campus de beauliau, RENNES cedex, 35042, France
Tal: 02.23.48.50.09
Fax: 02.23.48.50.20
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Mismatches:
Indels:
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Matches:
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
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TITLE
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  Indels:
Gaps:
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LGCKRYSYNNPGQVLPLKGPDOQTTSCLWHLQGPEDLMIKVRLEWTRVDCRDRVAMYD
PAGPIEKRLITSVYGCSRQEPVMEVLASGSVMAVVWKKGMEISYYDPFLLSVKSVAFQD
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VCDRQPDCLNGSDESQCQEGVPCGTFFFQCEDRSCVKKRPNPECDGQSDCRDGSDCOCC
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) RIKEN of Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohaman Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp, NRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9222,
                                                                             of 60,770 full-length Could be considered by the construction of 60,770 full-length Could be considered by the construction of 60,770 full-length Could be chases I to 3035)

Be deach, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Borly, F., Imeran, F., Hayatsu, N., Hiramoto, K., Hiracka, T., Horly, F., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomira, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Shibata, K., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tanaka, T., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Yoshida, K., Direct Subhission
                                             Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
        The FANTOM Consortium and the RIKEN Genome Exploration Research
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/db_xref="MGI:1904397"
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/strain="C57BL/6J"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                         163 AlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGlyAspValGln 182
                                                  362 GAGGACAGCACTACTACGCTGGCACTAATAGCTGGGTCACCGGATGGGGCGATATCAAT 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300008A22 product:hypothetical Serine proteases, trypsin family containing protein, full insert sequence. AKO04939
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                                                                                                                                                     422 AGIGAIGIGCCCCTICCCTCACCCGGGACCCTACAGGAGGIGACTGTGCCGGTAGTGGG
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                                                                                                                                                                                                                                                                                                              223 LeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAspThrCysGlnGlyAsp
                                                                                                     183 GlualaAspProleuProleuProTrpValleuGlnGluValGluLeuArgLeuLeuGly
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
Mus musculus
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Submitted, MD 20850, USA This sequence as made by sequencing genomic exons and ordering them
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VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                               2667 CCAGGGGCCAGCTAGGTTTCACTTCTAACCCTTTCTTATTCTAGTCTTTCCCC 2726
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1 (bases 1 to 2487)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                        2607 CCTACCCCAGTGACAGTACAGAGGATGTCAGCTGGTGGTTAGGATGCCTCCTGAGGT
                                                                                                                                                                             ---GlyVal SerThrGlyThrLysSerLeuVal---LeuProTrpLeuSerProHis---
                           --TCCAGGCCAAGTTCAGGGTGTCCACCC
                                                          LeuHisGlnThrAlaPheLeuAspSerAlaArgIleLeuLeuArgProLeuSer
SerGluProGlyProAlaPheProThrGlnProGlnLysThrGlnSerAspCys
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM7030"
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         DCGLOGLSSRIVGGTVSSEGEWPWQASLQIRGRHICGGALIADRWVITAAHCFQEDSM
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TVRPVCLDFARSHFFEBGQHCWITGMGAQREGGPVSNTLGKVDVQLVPQDLCSBAYRY
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RVTRVINWIQQVLT"
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/tissue type="embryo, stage 17/19"
/lab_host="DH10B (phage-resistant)"
/clone lib="NICHD XGC Emb2"
/note="Vector: pCWV-SPORT6; Site_1: Not1; Site_2: Sal1;
cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. Constructed by Life Technologies."
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                                                          Contact: Robert Strausberg, Ph.D.
Email: ggapbs-rémail.nih.gov
Tissue Profurement: Dr. Igor Dawid
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://mage.lnl.gov
Plate: LiAM10808 row: 1 column: 22
High quality sequence stop: 691.
       Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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/db_xref="taxon:8355"
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1660 AGCAAGGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAG 1719
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Mphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (Dases 1 to 905)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                              --SerAlaArgIleValGlyGlySerAsn
                                                                                                                                                                                                                                                                                                              92 AsnGly-----ThrLeuGluProAlaAlaGluTxpSerValLeuLeuGlyValHisSer
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                                                                                      1720 GACTGCGACTGTGGCTTGCGGTCATTCACGAGACAGGCTCGTGTTGTTGGGGGCACGGAT
                                                                                                                              AlaGlnProGlyThrTrpProTrpGlnValSerLeuHisHis---GlyGlyHisIle
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188 ProLeuProTrpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGln 207
         648 TCCATGTACGAAACCAGCTTGGGATACAAACCTAATGTTCCTTTT------- 692
                            208 CysLeuTyrSer------GlnProGly---ProPheAsnLeuThrLeuGln 221
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Search completed: February 25, 2004, 18:01:10 Job time: 2501 secs

Title: Perfect score:

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Minimum DB Maximum DB

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APPLICANT: Darrow, Andrew
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Andrede-Gordon, Patricia
APPLICANT: Qi, Jenson
TITLE OF INVENTION: DNA Encoding the Human Serine;
TITLE OF INVENTION: Protease EOS
FILE REFERENCE: ORT-1031
CURRENT APPLICATION VUMBER: US/09/387,375
CURRENT APPLICATION VUMBER: 1999-08-31
NUMBER OF SEQ ID NOS: 9
US-09-907-794A-262

US-09-905-125A-262

US-09-902-715A-262

US-09-902-71A-15

US-09-008-271A-15

US-09-008-271A-15

US-09-007-794A-256

US-09-005-715A-256

US-09-023-942A-5

US-09-023-942A-25

US-09-023-942A-25

US-09-023-942A-25

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US-09-023-942A-26

US-09-023-942A-28

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US-09-023-942A-28

US-09-038-642-9

US-09-016-366A-24

US-09-016-366A-24

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US-09-016-36A-20

US-09-016-36A-18

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Indels:
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Patent No. 6485957
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-MODEL=frame+ p2n.model -DEV=xlp
-Q=/CGT2_1/USFTO_spool_p/US.003441/runat_24022004_101039_17477/app_guery.fasta_1.519
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Sequence 30, Appl
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Sequence 8,
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11. /Ggn2_6/prodact2/lina/5A_COMB.seq:*
12. /Ggn2_6/prodacta/2/lina/5B_COMB.seq:*
33. /Ggn2_6/prodacta/2/lina/6A_COMB.seq:*
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6: /Ggn2_6/prodacta/2/lina/backfiles1.seq:*
                 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                            AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPro
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Sequence 8, Application US/09386642 Patent No. 6420157 GENERAL INFORMATION: APPLICANT: Darrow, Andrew

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Fusion general OTHER INFORMATION: with homo sapien serine protease catalytic domain US-09-386-642-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 GGGTGCTGTCACTGCTTCCCCAGGAGCACCACAAGGAA-----
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124
45
126
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Matches:
Conservative:
Mismatches:
APPLICANT: Qi, Jenson
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT APPLICATION NUMBER: US/09/386,642
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 1142
                                                                                                                                                                                                                                                                                                                                                                                                    US-10-037-417-46 (1-357) x US-09-386-642-8 (1-1142)
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                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                       1.7e-37
564.50
52.81%
38.75%
28.90%
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                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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ArgargasnargproGlyValPheThralaValAlaThrTyrGluAlaTrpIleArgGlu 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618 TACAGCAAAGACACCGAGTTTGGCTACCAACCCAAAACCATCAAGAATGACATGCTGTGC
                                                                                                                                                                                                                                                                                               AlaGlyTytProGluGlyArgArgArgThrCysGlnGlyAspSerGlyGlyProLeuVal
                                                                                                                                                                                                                                                                                                                  858 ATCATCCCCAAACTGCAGTTCCA-GCCAGCGAGGTTGGGCGGCCAGAAGTGAGACCCCCG
                                                                       GlyThrAlaCysTrpAlaThrGlyTrpGlyAspValGlnGluAlaAspProLeuProLeu
                                                                                                        CysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGly
                                  438 cccrrcaccaarracarccrcccccididicidecraccccrcdgrgarcrrraagacg
                                                                                                                                             ProTrpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCysLeu
                                                                                                                                                                                                                         TyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGly---MetLeuCys
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Dranac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 78461P2B
CURRENT FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 LeuHisGlnThrAlaPheLeuAspSerAlaArgIle 322
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Sequence 431, Application US/09620312D
Patent No. 6569662
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_F_genes Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Reiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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Wehrman, Tom
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APPLICANT:
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                                        261
                                                                                                                hrserPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThrAlaValAlaT 281
                                                                                                                                      301
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                                      lyAspSerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleT
                                                                                                                                                                                        hrjyrGluAlajrpijeArgGluGlnVajMetGlySerGjuProGlyProAlaPheProT
                                                                                                                                                                                                                                                                                     887 CCCAAACCCAGGAGTCCCCAGCCGACAGCAACCTCTGTGGCAACCTGGCCACCTGGCCTTC 942
                                                                           ergacrichegegecedacrerectecergregagegererengaracergaegedarre
                                                                                                                                                                                                                                                                301 hrGlnProGlnLysThrGlnSerAsp-----CysLeuHisGlnThrAlaPhe 316
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09386653A;
Patent No. 645864;
SERENAL INFORMATION:
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Darrow, Andrew
APPLICANT: Darrow, Andrew
TITLE OF INVENTION: DNA encoding the novel human serine;
TITLE OF INVENTION: DNA encoding the novel human serine;
TITLE OF INVENTION: DNA encoding;
TITLE REPERENCE: ORT-1032;
CURRENT APPLICATION NUMBER: US/09/386,653A.
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 1110
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Matches:
Conservative:
Mismatches:
Indels:
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563.50
51.28%
41.03%
28.85%
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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957 ATCATCCCCAAACTGCAGTTCCA-GCCAGGGAGGTTGGGCGGCCAGAAGTGAGACCCCCG 1015
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                                      ThrGlnProGlnLysThrGlnSerAspCys
                                                                                                                                                                 RESULT 5
US-09-023-942A-30
US-09-023-942A-30

Sequence 30, Application US/09023942A

Patent No. 6479274

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
                                                                 1016 eeecchegagccccrrraagcagagcrcrachcccccccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: POSIOL/97
FILING DATE: 13-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP0422/97
FILING DATE: 18-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: International PCT Application FILING DATE: 13-FEB-1998
ATTORNEY/AGENT INFORMATION:
ANNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980
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117
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                                                                                                                       1064 ---CACCATCCTGCTGGTCCTCCCAGCGCTGTT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/023,942A FILING DATE: 13-FEB-1998 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
                                                                                                    311 LeuHisGlnThrAlaPheLeuAspSerAlaArgIle 322
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                                                                                                                                                                                                                                                                                                              ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 GARDEN CITY PLAZA CITY: GARDEN CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 111.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742 4343
TELEFAX: (516) 742 4366
TELEFAX: (516) 742 4366
TELEFAX: 6510 742 4366
TELEFAX: 6510 742 4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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nucleic acid
                                       296 GlyProAlaPhePro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                       STATE: NEW YORK
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                                                                                                                                                                                                                                                                                                                                             252 GACACGCAGGAGGGCGAGTGGCCAAGTCAGCATCCAGCGCAACGGAAGCCACTTC 311
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Query Match:
          SEQ ID NO 431
LENGTH: 1212
TYPE: DNA
ORGANISM: HOMO S
                                                                                             NAME/KEY: CDS
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CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 1130
                                                            TYPE: DNA ORGANISM: Artificial Sequence
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557.00
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Best Local Similarity:
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Sequence 8, Application US/09387375

Patent No. 648595.

GENERAL INFORMATION:

APPLICANT: Darrow, Andrew

APPLICANT: Andrade-Gordon, Patricia

TITLE OF INVENTION: Drocase EOS

TITLE OF INVENTION: Protease EOS

TILLE OF INVENTION: Protease EOS

TILLE OF INVENTION: Protease EOS

TILLE OF INVENTION: NUMBER: US/09/387,375
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion gene
OTHER INFORMATION: with home sapien serine protease catalytic domain
OTHER INFORMATION:
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Matches:
Conservative:
Mismatches:
Indels:
                            Sequence 7, Application US/09386642;
Sequence 7, Application US/09386642;
Sequence 7, Application US/09386642;
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: Darrow, and and APPLICANT: Q1, Jenson
APPLICANT: Q1, Jenson
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
TITLE OF INVENTION: Zymogen Activation System
FILE OF INVENTION: Zymogen Activation System
FILE OF INVENTION: 27028
CURRENT APPLICATION NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-037-417-46 (1-357) x US-09-386-642-7 (1-1169)
                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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56.20%
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Sequence 1, Application US/09027337B

Sequence 1, Application US/09027337B

Sequence 1, Application US/09027337B

Seption No. 597261

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

APPLICANT: This indico, Histocomin Timoto, Histocomin Timing OF INVENTION: Breast and Ovarian Carcinomas

TITLE OF INVENTION: Breast and Ovarian Carcinomas

CURRENT APPLICATION NUMBER: US/09/027,337B

CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13
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ORGANISM: Homo sapiens
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2393 GTGGGCTTCCTCAGCGGCGCGTGAACTCCTGCCAGGGTGATTCCGGGGGACCCCTGTCC 2452
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                                                                 1763 AGCAAGGCAACCCTGAGTGTGACGGGAAGGAGGACTGTAGCGACGGCTCAGATGAGAAG 1822
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US-10-037-417-46 (1-357) x US-09-644-600-1 (1-3147)
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; Sequence 18, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotoshi
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         129 AlaAsnTyrSerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerPro 148
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                                                                                    149 AlaSerLeuGlyProAlaValTrpProValCysieuProArgAlaSerHisArgPheVal
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Sequence 1, Application US/09644600

Sequence 1, Application US/09644600

GENERAL INFORMATION:

APPLICANT: O'Brien, Timothy J.

APPLICANT: O'Brien, Timothy J.

TILE OF INVENTION: TAGG-15: An Extracellular Serine Protease

TILE REPERENCE: D664GIP/D;

CURRENT APPLICATION NUMBER: US/09/644,600

CURRENT FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR APPLICATION NUMBER: 09/421,213

PRIOR APPLICATION NUMBER: 09/027,337

PRIOR PELING DATE: 1999-02-20

PRIOR FILING DATE: 1998-02-20

MUMBER OF SEQ ID NOS: 98
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Mismatches:
Indels:
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2603 CCCAAATGTGTACAC 2617
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-644-600-1
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                                                                                                                                                                                            268 GlyArgArgAsnArgProGlyValPheThrAlaValAlaThrTyrGluAlaTrpIleArg
                               755 gradacirccrcagcadacaacaraaacrccraccaagaraarrccagagaacacaraca
                                                                                                                                                                                                                               695 AGCGTGGAGGCGGATGAGGCCGATCTTCCAGGCCGGTGTGGTGAGCTGGGGAGACGGGGGTGC
                                                                                     248 ValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCys
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
TITLE OF INVENTION: Overexpressed in Carcinomas
FILE REPRENCE: D664CIP/D
CURRENT APPLICATION NUMBER: US/09/654,600A
CURRENT FILING DATE: 2000-09-01
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Patent No. 6649741
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PRIOR FILING DATE: 1999-10-20
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                      TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease TITLE OF INVENTION: Overexpressed in Carcinomas FILE ERFRENCE: D6064CIP/D CURRENT APPLICATION WORDS: US/09/644,600 CURRENT FILING DATE: 2000-08-23 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR APPLICATION NUMBER: 09/421,213 PRIOR APPLICATION NUMBER: 09/027,337 PRIOR FILING DATE: 1998-10-20 PRIOR APPLICATION NUMBER: 09/027,337 PRIOR FILING DATE: 1998-02-20 NUMBER: 05 SEQ ID NOS: 98
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US-09-644-600-18
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ORGANISM: Artificial sequence
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   Conservative:
                                                                                 US-10-037-417-46 (1-357) x US-09-654-600A-18 (1-3147.
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                   Mismatches:
Indels:
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US-09-907-794A-262
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                      Gln----AspGlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValPro 128
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                                                                                                                                                                              209 LeuTyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCys
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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi; TITLE OF INVENTION: TAGG-15: An Extracellular Serine Protease; TITLE OF INVENTION: Overexpressed in Carcinomas; FILE REFERENCE: D6064CLF/D; CURRENT FILING DATE: 2000-09-01.
PRIOR FILING DATE: 2000-09-01.
PRIOR PELING DATE: 1999-10-20.
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2603 CCCAAATGTGTACAC 2617
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ORGANISM: Artificial sequence
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549.00
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NUMBER OF SEQ ID NOS:
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200 GITGIGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGAGCATCCAGAAG
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Godwark, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Sequence 262, Application US/09907794A Patent No. 6635468 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pari, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
                                                                                                                                                                           Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
                                                                                                                                                                                                                                                              Gerber, Hanspeter
Gerritsen, Mary E.
                                                                  APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Beton, Dan
APPLICANT: Beton, Dan L.
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ORGANISM: Homo Sapien
US-09-907-794A-262
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APPLICANT:
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LeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAspThrCysGlnGlyAsp 242
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Matches:
Conservative:
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PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-20
PRIOR PELING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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48.00%
35.73%
27.91%
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US-09-905-125A-262
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LENGTH: 1378
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MOOG, WILLIAM, 1.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: 10466-14
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR PRIOR PELICATION NUMBER: US 60/146,222
PRIOR PRIOR PELICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-11-29
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      955 TGGGGCCCTCAGGGCACCGAGCCAGGGCT-CTGGGGCCGCCGCGCGCTCCTAGGGCGCAG 1013
                                                                                                                       328 SerHisIleSerVal-----------GlyValSerThrGlyThrIysSerLeu 341
                                            308 SerAspCysLeuHisGlnThrAlaPheLeuAspSerAlaArgIleLeuLeuArgProLeu 327
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Patent No. 6664376
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Grimaldi, Christopher J.
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Wood, William, I.
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Stewart, Timothy A.
Tumas, Daniel
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Hillan, Kenneth, J.
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Filvaroff, Ellen
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Gerritsen, Mary E
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APPLICANT: Genentech, Inc.,
APPLICANT: BAShkenazi, Avi
APPLICANT: Botstein, David,
APPLICANT: Demoyers, Iuc.,
APPLICANT: Eaton, Dan L.
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Mather, Jennie P.
Pan, James
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
FRIOR PILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR REPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
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SerGlyGlyProLeuValCysGluGluGlyGlyArgTrpPheGlnAlaGlyIleThrSer 262
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Patent No. 6686451
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Goddard, A.
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Mather, Jennie P.
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Eaton, Dan L.
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APPLICANT: Ashkenazi, Avi
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Matches:
                   PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
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NUMBER OF SEQ ID NOS: 423
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APPLICATION NUMBER: PCT/US99/20594
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APPLICANT: PLOMMAN, GREGORY
APPLICANT: WHYTE, DAVID
APPLICANT: CAENEREEL, SEAN
APPLICANT: CAENEREEL, SEAN
APPLICANT: CHANYDCZAK, GIEN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
TITLE REFERENCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
CURRENT FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
SOFTWARE: PATENTIN VET: 2.1
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ORGANISM: Homo sapiens
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| cgn2 6/prodata/1/pubpna/USO7 PUBCOMB.seq:*
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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; Sequence 85, Application US/10176847; Publication No. US20030068636A1; GENERAL INFORMATION: ; APPLICANT: Veiby, Petter Ole

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TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY ITLLE OF INVENTION: AND OVARIAN CANCER FILE REFERENCE: MRI-039 CURRENT APPLICATION NUMBER: US/10/176,847 CURRENT FILING DATE: 2002-06-21 NUMBER OF SEQ ID NOS: 112 SOFTWARE: FREISEQ for Windows Version 4.0 SEQ ID NO 85.
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; ORGANISM: Homo
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
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CURRENT APPLICATION NUMBER: US/09/948,094
CURRENT FILING DATE: 2001-09-07
NUMBER OF SEQ ID NOS: 4
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Patent No. US20020090625A1

GENERAL INFORMATION:
APPLICANT: The Brigham and Women's Hospital, Inc.
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ORGANISM: Homo sapiens
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L41351
US-09-980-107-2214
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Matches:
Conservative:
Mismatches:
Indels:
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2214
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697.00
55.29%
42.33%
35.69%
                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
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Best Local Similarity:
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                                                            PheGlnAlaglylleThrSerPheGlyPheGlyCy9GlyArgArgAsnArgProGlyVal 275
859 CCTGAGGAGCCGCACTTTGTCCAAGAGGACATGGTGTGTGCTGGCTATGTGGAGGGGGGC 918
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                                 1264 GGCCCTACTTCCAGGATGGATGCATCACACTCAAGGACAGGAGCCTGGTCCTTC 1317
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Indels:
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John MONAHAN

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                                                                      LeulleAlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeu 95
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36 ProTyrCysGlyArgProGluProSerAlaArglleValGlyGlySerAsnAlaGlnPro
                                                   56 GlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySer
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Sequence 261, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:

US-10-097-340-261

RESULT 6

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and Proteins For The Identification, n, and Therapy of Ovarian Cancer
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Mismatches:
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Matches:
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CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT PILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR APPLICATION NUMBER: 60/24,967

PRIOR PILING DATE: 2001-03-14

PRIOR PILING DATE: 2001-03-14

PRIOR PILING DATE: 2001-03-6

PRIOR PILING DATE: 2001-03-6

PRIOR PILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR PILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR SPLING DATE: 2001-09-19

NUMBER: FASELSEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                     Assessment, Prevention,
                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules TITLE OF INVENTION: Assessment, Prevention
            Sebatian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
Manjula GANNAVARAPU
                                                                                                                                                       Peter VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
                                                                                                                                                                                                                                     Rosemarie SCHMANDT
Xumei ZHAO
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LENGTH: 1834
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TYPE: DNA

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gluproAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAsp 115
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CCTGAGGAGCCGCACTTTGTCCAAGAGAACATGGTGTGTGCTGCTGTATGTGGAGGGGGC
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GENERAL INFOGRATION:
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERRACE: 1517.0012
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 2001-03-20
NUMBER OF SEQ ID NOS: 805
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 48 74
LENGTH: 3382
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US-10-101-510-447
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                                 Alignment Scores:
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                  545 AAGGICAGCACCTGAAGGACAICCCCCACCCCAGCIACCTCCAGGAGGGCICCCAG
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
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         --CysLeuHis 312
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                                                                                                                                                                                                                                                                                                                                Sequence 208, Application US/09925301
Patent No. US20020052308A1
GENDERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 208
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LOCATION: (1565)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (1598)
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LOCATION: (1505)
OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity:
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US-09-925-301-208
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LeulleAlabroSerTrpValLeuSerAlaAlaHisCV8PheMetThrAsnGlyThrLeu 95
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Sequence 1, Application US/10109616
Publication No. US20030167484A1
GENERAL INFORMATION:
APPLICANT: Allen, Keith D.
TITLE OF INVENTION: ACTIVATING PROFERAE 1 (CAP1) GENE DISRUPTIONS
FILE REFERENCE: R-490
CURRENT APPLICATION NUMBER: US/10/109,616
CURRENT FILING DATE: 2002-03-28
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Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Gdinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
Smithson, Glennda
Gunther, Srik
                                                                                                  Zhong, Mei
Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles E
Guo, Xiaojia
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Suresh G
Kimberly
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Query Match:
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LENGTH: 1726
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PRIOR APPLICATION NUMBER: US 60/280,509
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: US 60/311,055
PRIOR FILING DATE: 2001-08-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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55.17%
41.38%
32.13%
                                                                                                                    TYPE: DNA ORGANISM: Mus musculus
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TITLE OF INVENTION: Droteins, Polynuclectides Encoding Them and Methods of TITLE OF INVENTION: Using the Same FILE REPERENCE: 21402-537

FILE REPERENCE: 21402-537

CURRENT APPLICATION NUMBER: US/10/042,865

CURRENT APPLICATION NUMBER: US/260,417

PRIOR APPLICATION NUMBER: 60/260,417

PRIOR PELING DATE: 2001-01-09

PRIOR PELING DATE: 2001-01-09

PRIOR FILING DATE: 2001-01-09

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-03-09

PRIOR PELING DATE: 2001-03-09

PRIOR PELING DATE: 2001-03-09

PRIOR PELING DATE: 2001-03-09

PRIOR PILING DATE: 2001-04-18

NUMBER OF SEQ ID NOS: 264

SOFTWARE: Patentin Ver. 2.1
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258 AlaglyileThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
                            278 AlavalAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyPro
                                                                                                                                                  962 CTGACTTCTACCTAGCTTCCTGGATCCACCACCATGTG-----GCAGAGCTCCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                            334 ValSerThrGlyThrLysSerLeu 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/10042865; Publication No. US20040029216A1 GENERAL INPORMATION: APPLICANT: Edigaru, Muralidhara APPLICANT: Eschusen, Bryan D APPLICANT: Casman, Stacie J APPLICANT: Shenoy, Suresh G; APPLICANT: Shenoy, Suresh G; APPLICANT: Spytek, Kimberly
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Grosse, William M
Aleobrook II, John P
Gerlach, Valerie L
Bdinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
Maryankar, Uriel M
Malyankar, Uriel M
Malyankar, Uriel M
Malyankar, Uriel M
Malyankar, Espelle
Payman, John
Smithson, Glennda
Gunther, Erik
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Gangolli, Esha A
Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
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Miller, Charles E
Guo, Xiaojia
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138 AlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpPro 157
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1012 GGTGTGTACACTCTGGCCTCTGTGGATCCAAAGAAGAAGGACTCTGCGGGA 1071
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AlaProSerTrpValLeuSerAlaAlaHisGYsPheMetThrAsnGlyThrLeuGluPro
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150 TGCGGGCAGCCCCGCATGTCCAGTCGATCGTTGGGGCCCGGGATGGCCGGGAACGAAGAAG
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                                                                                   254 ArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgArnArgPro
                           dlyargargargunrcysglnglyaspserglyglyproteuvalcysglugluglygly
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139
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129
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Sequence 1, Application US/10041400A

Publication No. US20020110895A1

GENERAL INFORMATION:
APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Of, Jenson
TITLE OF INVENTION: Drotease EOS
FILE REFRENCE: ORT-1031
CURRENT APPLICATION NUMBER: US/10/041,400A
CURRENT APPLICATION NUMBER: US/09/387,375
PRIOR APPLICATION NUMBER: US/09/387,375

PRIOR SEQ ID NOS: 9

SOFFWARE: Patentin Ver. 2.0
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Conservative:
Mismatches:
Indels:
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603.50
50.00%
39.27%
30.90%
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US-10-041-400A-1
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Best Local Similarity:
Query Match:
DB:
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                             61 CTTGGATTACTCCGGGTCGGGGGACAGGAGGGGAAGGGGAATGCCCAGATTGGT 120
                                                                                                                                                                                                                                                                                                                                                                       121 GTGGTGGAAACAGACACAGTTGTGGACTCCGGAACAATTGTGAGACTGGGCAGCATCGGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ArgProGlu----- 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               652 PACATCCGGCCCATCTGCCTCCTGCAGCCAACGCCTCCTTCCCCAACGGCCTCCACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 TTGCCAGACACTCCCTGCGGTGTGGCCCCCCAAGCACGCATCACAGGTGGCAGCAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnProGlyThrTrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGly
                                                                                                                                                                                                                                            1 ATGGCCCAGAAGGGGTCCTGGGGCTGGGCAGCTGGGGGCTGTGGCTAT
                                                                                                                                                                                                                                                                                    ----AsnSerAspSerTyrSerLeuTyrGly
                                                                                                                                                                                                                            MetalaGlnLysGlyValLeuGlyProGlyGlnLeuGlyAlaValAla
                                                                                               1161
134
45
121
70
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Conservative:
Mismatches:
Indels:
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                                                                                               Length:
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                                                                                                             612.00
48.38%
36.22%
31.34%
                                                                                                                                                                                                                                                                                                                                                  LeuVal-----
                      TYPE: DNA
CRGANISM: Homo sapiens
US-10-042-865-31
                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                      Alignment Scores:
Pred. No.:
                LENGIH: 1161
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GGCGACCTGGCACTGCAGCTGCGTCGCCCGGTGCCCCTGAGCGCTCGAGCGTCCAACCC	Alignment Pred. No.:	nt Scores:	
158 ValcysLeubroArgAlaserHisArgFneValHisSLYIMAlacysirpArdimety 177	Percent Simi Best Local S Ouerv Match:	Percent Similarity: Best Local Similarity Ouery Match:	:
178 TrpGlyAspValGlnGluAlaAspProLeuProTrpValLeuGlnGluValGlu	DB: US-10-0	DB: US-10-037-417-46 (1-357	(57)
LeuargieuleuGlyGlualaThrCysGlnCysieuTyrSerGlnBro	දුරු සි	38 CysGlyArg ¹ ::: 150 TGCGGGCAG	krg1
GlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGlu	ò	58 TrpProTr	j. L
681 CAGGCTGAGCGCATTGTGCTGCCTGGGAGTCTGTGTGCCGGGTACCCCCAAG 731	අු	210 redeceres	- <u>ö</u>
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254 ArgTrpPheGlnAlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgArgArgHr0 273 792 AgcTrGGTCGTGGTGGGCGTGGGCGAAGGTTGTGCCTGCCTGCCT	y da	98 ALAAIAGIU: 321 CCAGCTGAG	34G
	ò	118 HisThrArg	Arg
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294 Glu 296	ð	138 AlaAspLeu	Len -
912 GCTAGCCGGTGAGGCTGAAGCCAGCTGCTGGGGTCCCTCAGCCTCCTGGTTCATC 971	අුර	441 GGCGACCTG	-B
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972 CAGGCACCTGCCTATACCCCCACATCCCTTCTGCCTCGAGGCCCAAGATGCCTAAAAAAG 1029	gg		9
314 ralaPheLeuAspSerAlaArgIleLeuLeuArgProLeuSerHisIleSerValGlyVa 334 ::: ::: :::	<u>\$</u> 8	178 TrpGlyAsp 561 TGGGGCAGC	Asp AGC
1.SerThrGlyThrLysSerLeuValLeuProTrpLeuSer	λο	198 LeuArgieu	Leu
	qu	::: 621 GTGCCGCTG	- SE
348ProHisSerLeuLeuGlyLeuTrp 355	λŏ	214 GlyProPhe	Phe
1134 CCCAGGGAGTCACACTCCCTTGCTGTTT 1173	qu	681 CAGGCTGAG	GAG
RESULT 13	λõ	234 GlyArgArg	Arg
US-10-041-264A-1 Sequence 1, Application US/10041264A	ପ୍ର	732 GGCCACAAG	AAG
FUDILCALION NO. USZUJZZINAMA GENERAL INFORMATION:	δ	254 ArgTrpPhe	Phe
APPLICANT: Darrow, Andrew APPLICANT: Andrade-Gordon, Patricia	셤	792 AGCIGGGTC	GTG
APPLICANT: Q1, Jenson TITLE OF INVENTION: DNA Encoding the Human Serine	ò	274 GlyvalPhe	Phe
TITLE OF INVENTION: Procease bus FILE REFERENCE: ORT-1031	qa	852 GGGGTCTAC	ŢĀ
CURRENT FILICATION NUMBER: US/Lo/V4L,264A	δŏ	294 Glu	į
PRIOR FILITOR NUMBER: US/08/38/,5/5	qq	912 GCTAGCCGG	55
NUMBER OF SEQ 1D NOS: 9 SOFTWARE: PatentIn Ver. 2.0	δō	297	-Pro
LENGTH: 1613	qq	972 CAGGCACC	-0 -0
11rE: DNA 7 ORGANISM: Homo Bapiens	δ	314 rAlaPheLe	Je I e
1-4*0-01	QC	1030	į

nt Scores: 2.26e-45 Length: 1613 0.: 603.50 Matches: 139 Similarity: 50.00\$ Conservative: 38 cal Similarity: 39.27\$ Mismatches: 129 atch: 13 90\$ Gaps: 7	.7-417-46 (1-357) x US-10-041-264A-1 (1-1613)	38 CysGlyArgProGluProSerAlaArgIleValGlyGlySerAsnAlaGlnProGlyThr 57	58 TrpProTrpGlnValSerLeuHisHisGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGrLeuIle 77	CGCTCA	78 AlaProSerTrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluPro 97	98 AlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAla 11	CINCECCCCCCACG 38	118 HisThrArgAlaValAlaAlaileValValProAlaAsnTyrSerGlnValGluLeuGly 137 118 HisThrArgAlaValAlaIleValValProAlaAsnTyrSerGlnValGluLeuGly 137 119 HisThrArgAlaValAlaIleValValValProAlaAsnTyrSerGlnValGluLeuGly 137 119 HisThrArgAlaValAlaIleValValValValValValValValValValValValValV		CAACCC 50	158 ValcysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly 177	501 GICTGCCTGCCCGTGCCCGCCCGCCGCCCGCCCGGCACATGCCGGGTCACCGGC 560	178 TrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGlu 197	561 regegeraccrececeragastrececeteceragastregeearesetracaagastaags 620	198 LeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnPro 213	caccreceacecreraceaceresececes	214 GlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCysAlaGlyTyrProGlu 233	681 CAGGCTGAGCGCATTGTGCTGCCTGGGAGTCTGTGTGTGTGCGCTACCCCAG 731	234 GlyargargarghrCysGlnGlyAspSerGlyGlyBroLeuValCysGluGlyGly 253	732 Geccacaagacecraccagestaticagagacercracagacracagacragaga 791	254 ArgTrpPheGlnAlaGlylleThrSerPheGlyPheGlyCysGlyArgArgAsnArgPro 273	792 AGCTGGGTCCTGGTGGGGGGGGGGGGGGGGGGTTGTGCCCTGCCCAACGGTCGA 851	274 GlyvalPheThrAlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySer 293	acaccagnendeccacatanaececcnedatrcagecreecercrera	294 Glu	Ď	297ProAlaPhe-ProThrGlnProGlnLysThrGlnSerAspCysLeuHisGlnTh 314	972 CAGGCACCTGCCTATACCCCACATCCCTTCTGCCTCGAGGCCAAGATGCCTAAAAAAG 1029	314 rAlaPheLeuAspSerAlaArgIleLeuLeuArgProLeuSerHisIleSerValGlyVa 334	
Alignment Pred. No.: Score: Percent Si Best Local Query Matc	US-10-03	\$ 65	ò	QQ	දුරු පුර	ζ	Пр	8 8	a ·	상 점	ŏ	Db	ò	Db	δý	qu	ò	qq	à	qq	δλ	q	ζ	q ₀	οχ	qq	οχ	qq	ζō	qq

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us-10-037-417-46.p2n.rnpb

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972 CAGGCACCTGCCȚATACCCCACATCCTTCTGCCTCGAGGCCAAGATGCCTAAAAAAG- 1029
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                                                                                                                                                                                                                                                                                                                                                                      274 GlyvalPheThralavalAlaThrTyrGluAlaTrpIleArgGluGlnvalMetGlySer 293
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                                                                                                                                CAGGCTGAGCGCATT----GTGCTGCCTGGGAGTCTGTGTGCCGGCTACCCCAG
---SerGlnPro
                                     621 greccechéchéaachcececachchéceacesechchácaceresececesacerecec
                                                                                                                                                                               GlyArgArgAspThrCysGlnGlyAspSerGlyGlyProLeuValCysGluGluGlyGly
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  LeudrgieuleuGlyGludlaThrCysGlnCysleuTyr-
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Publication No. US20040005557A1
GENERAL INFORMATION:
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Colman, Steven D
Spytek, Kimberly A
Boldog, Ferenc
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Casman, Stacie J
Guo, Xiaojia Sasha
Edinger, Shlomit R
MacDougall, John R
Malyankar, Uriel M
Patturajan, Meera
Shimkete, Richada
Pena, Carol EA
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Herrman, John L
Peyman, John A
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Zerhusen, Bryan D
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Miller, Charles E
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APPLICANT: Darrow, Andrew
APPLICANT: Andrade-Gordon, Patricia
APPLICANT: Qi.Jenson
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TITLE OF INVENTION: Protease EOS
FILE REPERENCE: ORT-1031
CURRENT FILING DATE: 2002-01-08
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Taupier Jr, Raymond J
Gerlach, Valerie
Grosse, William M
Liu, Xiachong
Bllerman, Karen
Rothenberg, Mark
Stone, David J
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Kekuda,R., Alsobrook,J.P., Tchernev,V.T., Liu,X., Spytek,K.A., Patturajan,M., Grosse,W.M., Lepley,D.M., Burgess,C.E., Vernet,C.A., Li,L., Gorman,L., Edinger,S., Sciore,P., Ellerman,K., Malyankar,U., Rothenberg,M., Stone,D., Boldog,F., Shenoy,S. and Anderson,D. Proterins and nucleic acids encoding same Patent: WO 02053742-A 45 11-JUL-2002;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                             Plowman,G., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. Charydczak,G.
Novel proteases
Patent: WO 200860-A 52 03-JAN-2002;
Sugen, Inc. (US)
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272
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Conservative:
Mismatches:
Indels:
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272.00
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                             Homo sapiens (human)
Homo sapiens
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Query Match:
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                                          ORGANISM
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AX360096
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DEFINITION
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157 471 177 531 237

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PAT 13-FEB-2002

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BD127529 2810 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD127529
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PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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JP 2002017375-A/2960
22-JAM-2002
07-JTL-2000
JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                             TrpGlyAspValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGlu 197
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Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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Primer for synthesizing full-length cDNA and use thereof FH X
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GCCGACCTGGCCCTGCTGCCCTCACCCGCCAGCCTGGGCCCCGCCGTGTGGCCT
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Location/Qualifiers

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JP 2002017375-A/2960.
Homo sapiens (human)
Homo sapiens
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PN JP 200201737
PD 22-JAN-2002
PF 07-JUL-2000
PI ISHLI,
PI ISHLI,
PI YURI KAWAL, A
SHINICHI KOJIMA,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0245183-A 31 13-JUN-2002;

Incyte Genonics, Inc. (US)
                                                                                                              AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr
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Matches:
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Mismatches:
Indels:
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Sequence 31 from Patent WO0246383.
AX480935
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BD125219 670 bp DNA linear PAT 18-SEP-2002 Primer for synthesizing full-length cDNA and use thereof. BD125219.1 GI:23220164 JP 2002017375-A/650. Home appiers (human)
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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAXASHI, SHIZUKO
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Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Ota,T., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
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Primer for synthesizing full-length cDNA and use thereof Primer for synthesizing full-length cDNA and use thereof Primer for synthesizing full-length cDNA-2002;
Patent: JP 2002017375-A 650 22-JAN-2002;
BN JP 2002017375-A/650
PD 22-JAN-2002
PP 07-JUL-2000 JP 200253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, PI ISHII,
PI SHII,
PI YURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGA
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Matches:
Conservative:
Mismatches:
Indels:
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                                            1.59e-170
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Best Local Similarity:
Query Match:
DB:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                               297 irchidacdaaliddaacdciddaacccccccccadiddicdiddiacidcidddacdaca
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Regulation of human prostasin-like serine protease Patent: WO 0198467-A 1 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Sequence 1 from Patent W00198467.
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Homo sapiens
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AX342934/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlnAspGlyProLeuAspGlyAlaHisThrArgAlaValAlaAlaIleValValPro 128
Homo sapiens (human)
JP 2002017375-A/1916
22-JAM-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   OS Homo sapiens (human)
DE 20-2017375-A/1916
PD 22-3AN-2002
PP 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUJ PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINCHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC CIZNIS/09, CO7K14/47, CO7K16/18, C12NI/15, C12NI/19, C12NI/21, C12NI5/
                                                                                                                                                                                                   C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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/organism="Homo sapiens"
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Homo sapiens
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PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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1 (bases 1 to 670)

Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H.
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                                                                                           C C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 Primer for synthesizing full-length cDNA and use thereof FH K Location/Qualifiers
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                                                                                                                                                           /organism='Homo sapiens (human)'
Location/Qualifiers
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Matches:
Conservative:
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Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
          SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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Percent Similarity:
Best Local Similarity:
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1 (bases 1 to 127769)

DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                    85
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Homo sapiens chromosome 16 clone RP11-388M20, complete sequence.
AC009088
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                                   serine protease
                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
                 Xiao,Y. and Morozov,V.
Regulation of human prostasin-like ser
Patent: WO 0198467-A 3 27-DEC-2001;
Bayer Aktiengesellschaft (DE)
Location/Qualifiers
1. 456
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 GlyAspSerGlyGlyProLeuVal 248
24 GGTGACTCTGGGGGGCCCCTGGTC 1
                                                                                                                                                                                                                                                                                     US-10-037-417-46 (1-357) x AX342936 (1-456)
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DOB Joint Genome Institute.
Direct Submission
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128.00
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100.00%
35.85%
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Homo sapiens
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Submitted (193-APR-2002) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 127769)

ES DOB Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

LE Submitted (184-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

S (bases 1 to 127769)

ES (bases 1 to 127769)

ES (bases 1 to 127769)

ES (bases 1 to 127769)

LE Sind Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

LE Submitted (194-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Mar 20, 2003 this sequence version replaced gi:29029216.
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Homo sapiens chromosome 16 clone CTD-2551B20, WORKING DRAFT
SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GlyProblaValTrpProValCysLeuProArgAlaSerHisArgPheValHisGlyThr 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire sequence is 233.4kb). It is clipped at the overlap with AC135050.
The number of bases overlapped is 2575.
                                                                                                                                                                                                                                                                                                                                                                                                         www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 AenglyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHisSerGlnAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31589 AATGGGACCTGGAGCCCGCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31349 GCCTGCTGGGCCACCGGCTGGGAGAACGTCCAGGAGGCA 31311
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HTG; HTGS_PHASE1; HTGS_ACTIVEFIN.
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Mismatches:
Indels:
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100.00%
26.05%
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SOURCE

COMMENT

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AC106629 232119 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-21802, WORKING DRAFT SEQUENCE, 2
unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 SerGlnValGluLeuGlyAlaAspLeuAlaLeuLeuArgLeuAlaSerProAlaSerLeu
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873 101972: gap of unknown length

973 117076: contig of 15104 bp in length

1077 11717 gap of unknown length

1974 138973: contig of 21797 bp in length

1074 150336: contig of 11263 bp in length

1337 150336: gap of unknown length

1347 195476: contig of 45040 bp in length

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /clone="CTD-2551B20"
/clone_lib="CalTech human BAC library D"
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOD.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="16"
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100.00%
26.05%
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              101873
101973
117077
117177
138974
139974
150337
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Consensus quality: 18238 bases at least Q30
Consensus quality: 182638 bases at least Q30
Consensus quality: 188095 bases at least Q30
Consensus quality: 188095 bases at least Q30
Estimated insert size: 193376; sum-of-contigs estimation
Estimated insert size: 193376; sum-of-contigs estimation
Quality coverage: 7.63 in Q20 bases; agancise-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 22 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                             Unpublished
2 (bases 1 to 195476)
DOE Joint Genome Institute.
Direct Submission
Submitted (05-00T-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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gap of unknown length
contig of 12945 bp in length
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of 16423 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length
contig of 1595 bp in length
gap of unknown length
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of 4872 bp in length
unknown length
of 5717 bp in length
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of 9267 bp in length
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contig of 1136 bp in length
gap of unknown length
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of 6084 bp in length
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                                                                                                                                                                                Sequencing of Human Chromosome 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                         -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                1 (bases 1 to 195476)
DOE Joint Genome Institute.
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                      sapiens (human)
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                                                      Homo sapiens
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                                                      ORGANISM
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AUTHORS
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Draper H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls T., Fan, G., Francer, C., R., Gabisi, A., Garta, R., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garcia, M., Garca, M., Gabregorgis, E., Geer, K., Gill, R., Garcia, M., Garra, M., Gabregorgis, E., Geer, K., Gill, R., Garcia, M., Garra, M., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, K., Hernandez, J., Handels, S., Hldwis, M., Henderson, M., Hernandez, J., Greson, M., Hollins, B., Howells, S., Hldwis, M., Indianon, B., Johnson, R., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Johnson, K., Marchin, M., Marin, L., Kovar, C., Liu, W., Loulseged, H., Lozado, R.J., Lawis, L., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Liu, W., Martin, K., Martin, K., Martin, K., Martin, R., Mandom, B., Mandom, B., Mandom, B., Mandartne, M., Mandoud, M., Malloy, K., Mangum, B., Mandindartne, M., Mandoud, M., Malloy, K., Mangum, B., Mandindartne, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Munidasa, M., Morris, S., Shen, H., Saderer, A., Popovic, D., Primus, E., Pull, M., Ren, Y., Reuer, M., Rebe, R., Reilly, M., Ren, Y., Rever, M., Saderer, S., Soott, G., Shatsaan, S., Shen, H., Sheetty, J., Shuyartsbeyn, A., Sieson, I., Sitter, C., Smal, W., Shen, M., Shen, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M., Store, M
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Direct Submission

Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:23604383.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgum sequencing reads assembled using Atlas (http://www.hgsc.bcm.tuc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a' contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence on the sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgum sequence reads. Both end sequences and whole genome shotgum sequence reads. Both end sequences and whole genome shotgum sequence only contigs will be indicated in the feature
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3 (Dasses 1 to 232119)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GLSJ
Center clone name: CH230-21802
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Direct Submission
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AUTHORS
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COMMENT

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AC117170 244161 bp DNA linear HTG 15-NOV-2002 Rattus norvegicus clone CH230-20P9, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
AC117170
                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* COTE: This is a "working draft' sequence. It currently

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 244161)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
             Assembly program: Atlas 3.0;
Consensus quality: 222629 bases at least Q40
Consensus quality: 222625 bases at least Q30
Eschessing quality: 224449 bases at least Q20
Estimated insert size: 234994; sum-of-contigs estimation
Quality coverage: 9x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114340 TCCCTCATGGCCCCTTCCTGGGTCCTCTCGGTGCTGTTTC 114296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 SerLeulleAlaProSerTrpValLeuSerAlaAlaHisCysPhe 89
                                                                                                                                                                                                                                                                                                                                                                                           230792 230891: contig of 230791 bp in length 230792 230891: gap of unknown length 230892 232119: contig of 1228 bp in length. Location/Qualifiers 1. 232119 /organism="Rattus norvegicus"
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Rattus norvegieus (Norway rat)
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Matches:
Conservative:
Mismatches:
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Summary Statistics
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128621. .230127
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Best Local Similarit
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Anyalebechi, V., Aoyagi, A., Modekji, W., Baras, E., Badon M., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Barashand, P., Charle, J., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M., Charles, M.,
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REFERENCE AUTHORS TITLE JOURNAL

TITLE JOURNAL AUTHORS TITLE

JOURNAL

COMMENT

REFERENCE

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data.html).
                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.)

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 5 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25619: contig of 25619 bp in length 25719: gap of unknown length 137872: contig of 112153 bp in length 137972: gap of unknown length 240790: contig of 102818 bp in length 240890: gap of unknown length 241970: contig of 1080 bp in length 242070: gap of unknown length 242070: gap of unknown length 242070: gap of unknown length 242070: gap of unknown length
                                                 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
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Center: Baylor College of Medicine Center code: BCM
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                          129868 CCTGGCRCTTGGCCGTGGCAGGTGAGCCTGCATCACGGTGGAGGCCACATCTGCGGGGGC 129927
                                                                                                                                                                                      AC093520 168064 bp DNA linear PRI 19-MAR-2003
Homo sapiens chromosome 16 clone RP11-120K18, complete sequence.
AC093520
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hinishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission

Submitted (11-AUG-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Dose Joint Genome Institute.

Direct Submission

Direct Submission

Mitchell Drive, Walnut Creek, CA 94598, USA Direct Submitted (13-UN-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (bases I to 168064)

DOE Joint Genome Institute.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JUL-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 5 (Dases I to 188064)
DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 168064)

2D Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.

Direct Submission

Unpublished
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74
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                                                                                                   129928 FCCTCATGGCCCTTCCTGGGTCCTCCGCTGCTGTTTC 129972
                                                                                  SerLeuileAlaProSerTrpValLeuSerAlaAlaHisCysPhe
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DOE Joint Genome Institute.
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Oy 312 HisGlnThrAlaPheLeuAspSerAlaArgIleLeuLeuAgProLeuSerHisIleSer 331

Db 141592 CATCAAACGGCATTCTGCCAGAATCCTTTTGAGGCCTTGTCCCATATATCA 141533

Qy 332 ValGlyValSerThrGlyThrLysSer 340

Db 141532 GTAGGAGTCTCAACTGGGACCAAAAGC 141506
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Search completed: February 25, 2004, 23:28:10 Job time : 3995 secs

Human pro DNA encod

Nucleotid

Human cDN Human pro

Human ner Human NOV

Human NOV

OM protein

Run on:

Sequence:

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Human, NOVX, neurological disorder; Alzheimer's disease;

Huntington's disease; Parkinson's disease; pain; behavioural disorder;

Huntington's disease; Parkinson's disease; pain; behavioural disorder;

Mutoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

Mutoimmune disease; myasthenia gravis; asthma; arthritis; diabetes;

Mutoiditis; cardiovascular disease; hypertension; reproductive disorder;

Myarciditis; cirrhosis; glomerular endotheliosis; bacterial infection;

Myarciditis; call signal processing-related disorder;

Myarciditis and processing related disorder;

Myarcininflammatory; immunosuppressive, analgesic; antiatherosclerotic;

My dermatological, antibacterial; antiathritis; hepatotropic; neuropprotective;

My differentiation, proliferation; morility; heematopoiesis; wound healing;

My and progressive forensic biology; transgenic animal; drug screening;

My gene therapy; NOV14a; prostatin precursor-like; chromosome 16; gene; ds.
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Ada50520 1
Add09102 1
Aax80905 1
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Aas85946
Ada05701
Aaz44182
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Abz35510 |
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Ab167949 o
Ab168512 l
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Abn95716
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Ada05699
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Abn85393
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ABN85393
ABN85392
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ABK12241
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ADA05691
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ADA50520
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AAS85946
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AAZ11029
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AAV84052
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   Command line parameters:
-MODEL=frame+p2n.model -DBV=x1p
-MODEL=frame+p2n.model -DBV=x1p
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-NO WARP -LARGEQUERY -NEG SCORES=0 -MAXIT -BSPBELCK=100 -LONGIGG
-DBT TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELDEP=7
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3619.586 Million cell updates/sec
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1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
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Aak94500 I
Abk13565 I
Aa869040 I
Aak92190 I
               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                        - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                               3373863 seqs, 2124099041 residues
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Human neu Human ser Human ser

Human NOV

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Human lat Human gen Human NOV

Ovary can Kidney ca Kidney ca CDNA enco Gene #221

CDNA enco Human bre Human ova

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The invention relates to 24 novel human proteins designated NOV1-NOV14 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and nucleic acids encoding them (ABQ93879-ABQ93902). NOVX proteins and collectides are useful in the meantacture of a medicament for treating such disorders are associated with specific applications described for each of the 24 (SOVX proteins, based on their homology to known proteins. Various disorders are associated with NOVX proteins including neurological disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), colorectal cancer, leukaemia and osteosarcoma), immune disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), colorectal cancer, leukaemia and osteosarcoma), immune disorders (e.g., allergies and autoimmune disoraces, endometriosis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, asthma, continence, psoriasis, scleroderma, alopecia, ulcers, pancreatitis, dispertension), reproductive disorders, endometriosis, colorectal cancer, and particularly cardiomyopathy, atherosclerosis, cell signal processing-related disorders and disorders of metabolic pathway regulation. NOVX nucleic acids and polypeptides may be used to identify cellular receptors or domestream effectors which confidentification of small molecules that modulate or inhibit processes such indentification, haematopoiesis, wound healing and angiogenesis. NoVX nucleic acid sequences can be used to identifying and cloning NOVX homologues in other cell or producing non-human comprising NOVX nucleic acids are useful for studying the function and are useful as a source of primers or probes for forensic biony and comprising only more are useful for studying the function and cransgenic animals which are useful for studying the function and conjugated are useful for producing non-human comprehenses and polypers are useful for producin
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/product= "NOV14a"
/note= "No stop codon given in the specification"
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08-JAN-2001; 2001US-0260360P.
28-FBB-2001; 2001US-0272411P.
02-WAR-2001; 2001US-037321P.
05-JUL-2001; 2001US-0305060P.
12-JUL-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318405P.
12-SEP-2001; 2001US-0318400F.
04-JAN-2002; 2002US-0318100P.
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                                                     321 ArgileleuleuArgProleuSerHisileSerValGlyValSerThrGlyThrLysSer 340
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Patturajan M, Grosse WM, Lepley DM, Burgess CE, Vernet CAM, Li I
Gorman L, Edinger S, Scioce P, Ellerman K, Malyankar U;
Rothenberg W, Stone D, Boldog F, Guo X, Shenoy S, Anderson D;
Padigaru M, Taupier RJ, Miller CE, Eisen A;
1039 CTTGTCCTCCCCTGGCTCTCTCCACACTCTCCTGGGCCTCTGGGGGTTC 1089
                                                                                      Human; NOVX; neurological disorder; Alzheimer's disease;
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28-FEB-2001; 2001US-0272411P.
02-MAR-2001; 2001US-0272817P.
05-JUL-2001; 2001US-0393231P.
12-JUL-2001; 2001US-031840SP.
12-SEP-2001; 2001US-031840SP.
12-SEP-2001; 2001US-031840SP.
04-JAN-2002; 2002US-00037417.
                                                                                                                                                                ABQ93902 standard; DNA; 1102 BP.
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Gorman L, Edinger S, Sc.
Rothenberg M, Stone D, 1
Padigaru M, Taupier RJ,
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79 TACTCACTITACGGGTTGGGGCCGTCCGGACCCGCTAGGGGCCCCCGGTACTGGGGCCC

21

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78

19 ATGGCCCAGAAGGGGGTCCTGGGGCCTGGGCAGCTGGGGGCCTGTGCCAATTCTGACTCA TyrSerLeuTyrGlyLeuValProSerGlyProAlaArgGlyProProTyrCysGlyArg

MetalaglnLysGlyValLeuGlyProGlyGlnLeuGlyAlaValAlaAsnSerAspSer

357 0 0 0 0

Matches: Conservative: Mismatches: Indels:

357.00 100.00% 100.00%

Gaps:

(1-1102)

Length:

259 idderictrictectecrearierirandareaandeakeirideakeeteeteekeeks 318

81 TrpValLeuSerAlaAlaHisCysPheMetThrAsnGlyThrLeuGluProAlaAlaGlu 100

61 GlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIleAlaProSer

41 ProGluProSerAlaArgileValGlyGlySerABnAlaGlnProGlyThrTrpProTrp

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The invention relates to 24 novel human proteins designated NOVJ-NOVJ4 (ABB09501-ABB09524), collectively referred to as NOVX proteins, and nucleic acids encoding them (ABQ9879-ABQ993902). NOVX proteins, and nucleic acids encoding them (ABQ9879-ABQ993902). NOVX proteins, and nucleic associated disorders or in the manufacture of a medicament for treating such disorders with specific applications described for each of the 24 (NOVX proteins, based on their homology to known proteins. Various disorders (e.g., Alzheimer's, Huntington's and Parkinson's diseases), disorders (e.g., allergies and autoimmune diseases), myasthenia gravis, cancers (e.g., allergies and autoimmune diseases), myasthenia gravis, asthma, various forms of arthritis, diabetes, thyroiditis, cardiovascular disease (e.g., hypertension), reproductive disorders, endometriosis, incluned gravis, asthma, incontinence, peoriasis, scleroderma, alopecia, ulcers, pancreatitis, diabetes, thyroiditis, cardiovascular disease, cirrhosis, glonerular endotheliosis, polycystic kidrey disease, endocrine disorders, obesity, bacterial infections and particularly cardiomyopathy, atherosclerosis, call signal processing-related disorders and disorders of metabolic pathway regulation. NoVX nucleic acids and polycytic call and are also useful as targets for the binds to a NOVX protein, and are also useful as targets for the binds to a NOVX protein, and are also useful as targets for the profession call sequences can be used to identify acell notiliar copensor or probes for forensic piology and for identifying and cloning NOVX homologues in other cell types. Cells comprising NOVX nucleic acids are useful for studying the function and craning and for identifying and eloning NOVX homologues in other cell types. Cells are identifying and cloning NOVX homologues in other cell types. Cells are inversed and for identifying and eloning NOVX homologues in other cell types. Cells are intervaled.
                                                                                   Novel polypeptides and nucleic acids homologous to transmembrane receptor, thymosin, neuromodulin-like family of proteins for diagnosing, treating cancer, atherosclerosis, neurological, skin and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity of NOVX proteins and for identifying and evaluating mo of NOVX activity. The present sequence represents DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1102 BP; 162 A; 371 C; 353 G; 216 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostatin precursor-like protein NOV14b
                                                                                                                                                                                                                                                                                                                                                                                             Claim 9a; Page 143; 323pp; English.
P-PSDB; ABB09524
                                                                                                                                                                                                                                                                                       disorders.
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Caenepeel

Manning G,

Sudarsanam S,

Whyte D,

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The present invention relates to the isolation of novel human proteases, and the nucleic acids encoding them. The sequences of the invention are useful for treating diseases and disorders such as cancers (e.g. breast, colon, lung), immune-related diseases and disorders (e.g. inflammatory diseases and asthma), cardiovascular diseases (e.g. restenosis and disorders (e.g. inflammatory thrombosis), brain or neuronal-associated diseases, metabolic coronary thrombosis), brain or neuronal-associated diseases, metabolic rheumatoid arthritis and psoriasis), central or peripheral nervous system circumatoid arthritis and psoriasis), central or peripheral nervous system disorders, metabolic diseases, migratines, pain, sexual dysfunction, mood disorders, attention disorders (e.g. Alzheimer's disease, Parkinson's disease, and psorporial disorders (e.g. Alzheimer's disease, Parkinson's disease) and dyskinesias. The nucleic acids and polypeptides are also useful for treating viral infections such as ocular disease (e.g. virus (HIV), and non-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (e.g. virus (HIV), and mon-viral infections such as ocular disease (e.g. virus (HIV)).
                                                                                                                                                                                                      Nucleic acids encoding novel human proteases, useful for useful for treating diseases and disorders such as cancers, immune-related diseases and disorders, cardiovascular disease (e.g. restenosis) and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences encoding for the novel human proteases of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2457 BP; 377 A; 851 C; 797 G; 432 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  Claim 26; Fig 18S-TT; 313pp; English
                                       26-JUN-2001; 2001WO-US020171
                                                                  26-JUN-2000; 2000US-0214047P
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                                                                                                                               AlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpProValCysLeu
                                                                                                                                                                                       ProArgalaSerHisArgPheValHisGlyThralaCysTrpAlaThrGlyTrpGlyAsp
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                                                                                                                                                 TrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAlaHisThrArg
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                                                                                          38 CysGlyArgProGluProSerAlaArg11eValGlyGlySerAsnAlaGlnProGlyThr
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    2457
272
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0
               Matches:
Conservative:
Mismatches:
     Length:
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               272.00
100.00%
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Alignment Scores:
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Human; protease; cancer; immune-related disorder; cardiovascular disease;

encoding novel human protease #52.

(first entry)

23-APR-2002

ABK31795

BP

ABK31795 standard; DNA; 2457

neuronal associated disease; metabolic disorder; inflammatory disorder; nervous system disorder; sexual dysfunction; pain; mood disorder; hypertension; psychotic disorder; neurological disorder; dyskinesia; viral infection; human immunodeficiency virus; HIV; non-viral infection;

ocular disease; cytostatic; gene; ds.

WO200200860-A2 Homo sapiens

Swarnakar A; Elliott VS;

Griffin JA,

Au-Young J, Ellic Lu DAM, Lee EA; MG, Khan FA;

Delegeane AM, Yao MG,

Warren BA, Baughn MR, Gandhi AR,

Kallick DA, Bar Hafalia AJA, Ga

Azimzai Y, Walia NK,

Yue H, Lal PG,

Thangavelu K, i, Arvizu C, D

Lal Fo, Ramkumar J, The Sanjanwala MM; WPI; 2002-519664/55.

P-PSDB; ABB98135

08-DEC-2000; 2000US-0254399P. 21-DEC-2000; 2000US-0257603P. 05-UAN-2001; 2001US-0260110P. 19-UAN-2001; 2001US-02681P. 25-UAN-2001; 2001US-0264623P.

(INCY-) INCYTE GENOMICS INC

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237
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The invention relates to an isolated Protein Modification and Maintenance (PMM) polypeptide. Polypeptides of the invention may be used in the diagnosis, treatment and prevention of disorders associated with decreased expression or activity of PMM. These include gastrointestinal disorders (e.g. Crohn's disease), cardiovascular disorders (e.g. typertension), autoimmune/inflammatory disorders (e.g. anaemia), cell hypertension), autoimmune/inflammatory disorders (e.g. anaemia), cell proliferative disorders, developmental disorders (e.g. Alzheimer's disease) reproductive disorders (e.g. Alzheimer's disease) reproductive disorders (e.g. Alzheimer's disease) accine for such diseases. They may also be used in the assessment of the effects of exogenous compound on the expression of nucleic acid and amino acid sequences of protein modification and maintenance molecules. The current sequence represents a human PMMM encoding sequence of the invention, encoding a polypeptide which has been found to have homology
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                                                                                                                                                                                                                                                                                                        ThrCysGlnGlyAspSerGlyGlyBroLeuValCysGluGluGlyGlyArgTrpPheGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                278 AlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyPro
                                                                                                                         ACCTGCCAGGGTGACTCTGGGGGGCCCCTGGTCTGTGAGGAAGGCGGCCGCTGGTTCCAG
                                                                                                                                                                                                                                                                                                                                                                             AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgFroGlyValPheThr
                                ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
                                                                                                 TrpGlyAspValGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGlu
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                                                                                                                                                                                                                                                           CTCACTCTCCAGATATTGCCAGGGATGCTGTGTGTGCTGGCTACCCAGAGGGCCGCAGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 GCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCTGGGCCT
GCCGACCTGGCCCTGCTGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCCGCCGTGTGGCCT
                                                                                                                                                                    LeuArgLeuLeuGlyGluAlaThrCysGlnCysLeuTyrSerGlnProGlyProPheAsn
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K, Kojima S, Otsuki T, Koga
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and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic cancer; lipid accumulation; osteoporosis; Paget's disease; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
used to modulate, frame activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (Cop), atherosclerosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a therappeutic target of decreasing human prostasin-like serine protease activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the mucleotide sequence may be used to mimic,
                                                                                                                                                                                                                                                                                                                     antiatherosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention comprises the cDNA and protein sequences of an isolated prostasin-like serine protease and reagents and methods for regulating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease purified from human seminal fluid. An antibody specific for prostasin-like serine protease is useful for immunodetection and diagnosts of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of
                                                                                                                                                                                                                                                                                                                Human, prostasin-like serine protease, cytostatic, antiatherosclerotic
virucide, osteopathic, antiinflammatory, vasotropic, neuroprotective,
trypsin-like, metastasis, autoimmune lesion, atherosclerosis, gene,
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/partial
                                                                                                                                                                                                                                                                          Human prostasin-like serine protease cDNA #1.
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P-PSDB; AAU75082.
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augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serine protease activity inhibits both smooth muscle cell proliferation
                                                             and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to
                                                                                                                   diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #1 nucleotide sequence of the invention
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                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed care in diagnostics as expressed sequence tags for identifying expressed care in diagnostics of the control of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for sepressing (II). (I) and (II) are useful for treating disorders or supplement. (II) and its binding partners are useful in medical imaging control abstract protein expression or biological activity. The prolypeptide and polynucleotide sequences have applications in displaymentics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and an original activity. The mapping and the products dependent on DNA and an original activity and applications in the product of the types of data and products dependent on DNA and and an original activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 GCCAGCCTGGGCCCCGCCGTCTGCTGCCTGCCCCCGCGCCTCACACGCTTCTGTG
                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 597 BP; 97 A; 217 C; 196 G; 87 T; 0 U; 0 Other;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4844; 103pp; English
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                                                                                                                                                                         Tang YT;
                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                      30-MAR-2001; 2001WO-US008631
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P-PSDB; ABG04853
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                                                                                                                                                                                                                                                                                              biodiversity.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers anable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     una provided in the invention. Note: The sequence of the S'-end of not form part of the printed specification, but was obtained in CD-format directly from BPO
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                                                                                                228
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                                              351
                                                                                                                             LeuProftpValLeuGlnGluValGluLeuArgLeuLeuGlyGluAlaThrCysGlnCys
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                                                                                                LeuTyrSerGlnProGlyProPheAsnLeuThrLeuGlnIleLeuProGlyMetLeuCys
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a T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
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Mismatches:
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02-MAY-2000; 2000JP-00183765.
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Wakamatsu A, Sugiyama T,
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representative sequence

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                                                                                         PheMetThrAsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHis 108
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                                                                                                        357 TCCCAGGACGGGCCCCTGGACGGCGCGCACCCGCGCGCAGGGCCGCCATCGTGGTGCCG
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            1177 GGGGGCTCAAACGCGCAGCCGGGCACCTGGCCTTGGCAAGTGAGCCTGCACCATGGAGGT
                                                        237 GGCCACATCTGCGGGGGGCTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGCTGTGT
GlyGlySerAsnAlaGlnProGlyThrTrpProTrpGlnValSerLeuHisHisGlyGly
                                             GlyHisIleCysGlyGlySerLeuIleAlaProSerTrpValLeuSerAlaAlaHisCys
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S, Otsuki T, Koga
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K, Kojima
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su A, Sugiyama T, Nagai
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02-MAY-2000; 2000JP-00183765.
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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special

830 Primers useful for synthesizing full length cDNA clones and their use

genetic manipulation.

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WPI; 2001-524255/58.

Example 11; SEQ ID NO 1916; 1380pp + Sequence Listing; English.

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Human; prostasin-like serine protease; cytostatic; antiatherosclerotic; virucide; osteopathic; antiinflammatory; vasotropic; neuroprotective; trypsin-like; metastasis; autoimmune lesion; atherosclerosis; gene; renal failure; malignant cell; tumour angiogenesis; enzyme; inflammation; chronic obstructive pulmonary disease; COPD; restenosis; atherosclerosis; neurodegenerative disease; prion protein; infection; amyloid plaque; Genstmann-Straussler Syndrome; viral infection; Scrapie; Creutzfeldt-Jakob disease; metastatic_cancer; lipid_accumulation;
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methods. The present sequence was used as the representative sequence
from a human clone which was used in homology searches to identify the
clone. Note: The sequence data for this patent did not form part of the
printed specification, but was obtained in CD-ROM format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheMetThrAsnGlyThrLeuGluProAlaAlaGluTrpSerValLeuLeuGlyValHis
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Matches:
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This invention comprises the cDNA and protein sequences of an isolated protestasin-like serine protease and reagents and methods for requlating the human prostasin-like enzyme activity. Prostasin is a trypsin-like serine protease is useful for immunodetection and ingnosis of micro-metastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples and body fluids. The antibody may be used to modulate enzyme activity in a disease, such as metastasis of malignant cells, tumour angiogenesis, inflammation, chronic obstructive pulmonary disease (COPD), atheroscierosis, neurodegenerative disease (e.g. prion protein amyloid plaques of Genstmann-Straussles Syndrome, creutzfeldt-Jakob disease, Scrapie) or infection, particularly viral infection. The human prostasin-like serine protease gene provides a chimic, in particular for treates and protein ample of decreasing human protease gene provides a chimic, in particular for treates and protease and protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protein ample of the protei
                                                                                                                                                                                                                                                                                                                                                                                       Novel human prostasin-like serine protease polypeptide and polynucleotide which can be regulated for treating metastasis of malignant cells, inflammation, atherosclerosis, neurodegenerative disease and infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity, in particular for treating or preventing metastatic cancer. The agonists and antagonists of the nucleotide sequence may be used to mimic, augment and inhibit the enzyme activity which may be useful to treat osteoporosis, Paget's disease and degradation of bone implants particularly dental implants. Altered levels of human prostasin-like serime protease activity inhibits both smooth muscle cell proliferation and lipid accumulation and inhibit the progression of restenosis and atherosclerosis. The nucleic acid sequence is also useful in diagnostic assays for detecting diseases and abnormalities or susceptibility to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases related to the presence of mutations in nucleic acid sequences which encode the enzyme. The present sequence represents the human prostasin-like serine protease #2 nucleotide sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 3; 111pp; English
                                     23-JUN-2000; 2000US-0213588P.
20-MAR-2001; 2001US-0276909P.
                                                                                                                                                                                                                                                                                                                    WPI; 2002-114576/15
                                                                                                                                                                                                                                     Morozov V;
                                                                                                                                                      (FARB ) BAYER AG
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                                                                                                                                                                                                                                     Xiao Y,
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Sequence 456 BP; 74 A; 151 C; 167 G; 62 T; 0 U; 2 Other;

201 LeuglyGlualaThrCysGlnCysLeuTyrSerGlnFroGlyProPheAsnLeuThrLeu 220 161 ProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGlyAsp 180 12.1 AlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeuGlyAlaAspLeu 141 AlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpProValCysLeu 324 GCCCTGCTGCGCCTGGCCTCACCCGCCAGCCTGGGCCCCGCGCGTGTGGCCTGTCTGCCTG 264 CCCCGCGCCTCACACCCCTTCGTGCACGCCCCCCCTCGCTGGGCCACCGGCTGGGAGAC 181 ValGlnGluAlaAspProLeuProLeuProTrpValLeuGlnGluValGluLeuArgLeu Matches: Conservative: Mismatches: Indels: Length: US-10-037-417-46 (1-357) x ABK13566 (1-456) 3.37e-108 128.00 100.00% 100.00% 35.85% Best Local Similarity: g ò g ò à g à g

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221 GlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgAkgAspThrCysGln
144 CTGGGCGAGGCCACCTGTCAATGTCTTACAGCCAGCCCGGTCCCTTCAACCTCACTTT
                                                                                                                                                                                     Human, chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                     DNA encoding novel human diagnostic protein #6883.
                                                      241 GlyAspSerGlyGlyProLeuVal 248
                                                                 24 GGTGACTCTGGGGGGCCCCTGGTC
                                                                                                              AAS71079 standard; cDNA; 2298
                                                                                                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                           Tang YT;
                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                           Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABG06892
                                                                                                                                                                                                                                     WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity.
                                                                                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                        11-OCT-2001
                                                                                                                                 AAS71079;
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Claim 1; SEQ ID NO 6883; 103pp; English

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGN) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics for sense types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 2298 BP; 468 A; 774 C; 706 G; 350 T; 0 U; 0 Other;

Alignment Scores:

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483
                                                                                                                                                                                              AlaValAlaThrTyrGluAlaTrpIleArgGluGlnValMetGlySerGluProGlyPro 297
                                                                                                                                                                                                                            GCTGTGGCTACCTATGAGGCATGGATACGGGAGCAGGTGATGGGTTCAGAGCCTGGGCCT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted polypeptide; nervous disease; muscular disease; tumour; gastrointestinal ulceration; spinal cord disease; trachea disease; thyroid gland disease; ovary disease; prostate disease; heart disease; renal gland disease; small intestine disease; thymus disease; lymph node disease; muscular system disease; colon disease; lipase deficiency; cystic fibrosis; pancreatitis; clot formation; microbial infarction; angioplasty; liver disease; coagulation disorder; microbial disease; immune disorder; inflammation; transplant rejection; bone thickness; bone density; ferroxidase loss; apoptosis; vascular smooth cell proliferation; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated secreted polypeptide useful for treating nervous and muscular diseases, gastrointestinal ulceration, coagulation and immune disorders, microbial diseases, inflammation and transplant rejection.
                                                                                                                                  Xiang
                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human secreted polypeptide.
                                                                                                                                                                                                                                                          AlaPheProThrGlnProGlnLysThrGlnSerAsp 309
                                                                                                                                                                                                                                                                                   GCCTTTCCCACCCAGAGACCCAGTCAGAT 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "secreted polypeptide"
 Length:
Matches:
Conservative:
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                                               Mismatches:
                                                           Indels:
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                                                                                                       (1-2298)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                       US-10-037-417-46 (1-357) x AAS71079
                                                                                                                                                                                                                                                                                                                                                  BP
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13-MAR-2000; 2000US-0188916P.
03-OCT-2000; 2000US-0236874P.
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9.73e-38
52.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-570768/64.
                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                   424
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                                                          Query Match
DB:
   Pred. No.:
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                 Score:
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The present sequence encodes a human secreted polypeptide. The secreted polypeptides and polymucleotides are useful for treating nervous and muscular diseases, for inhibiting tumour formation and metastasis, for treating gastrointestinal ulceration, for preventing and treating diseases in spinal cord, thyroid gland, ovary, prostate, renal gland, consmall intestine, heart, trachea, thymus, lymph node, muscular system and colon, for treating lipase deficiency in cystic fibrosis and paraction, during angioplasty and all surgical procedures that require decreased blood clot formation, for treating liver diseases, coagulation disorders and microbial diseases, for treating lineametion and transplant rejection, for enhancing bone thickness and increasing bone density, for reducing the loss of essential ferroxidases, for suppressing apoptosis, and for regulating vascular smooth cell proliferation. They may also be used as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGAGGTGGCCACATCTGCGGGGGGCTCCCTCATCGCCCCCTCCTGGGTCCTCTCCGGCTGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GlyGlyGlyHisIleCysGlyGlySerLeuIleAlaProSerTrpValLeuSerAlaAla 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human nervous system related polynucleotide SEQ ID NO 13567.
                                                                                                                                                                                                                                                                                       Sequence 768 BP; 125 A; 280 C; 224 G; 139 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                         768
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Matches:
Conservative:
Mismatches:
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2000US-0184664P.

2000US-0186350P.

2000US-0189874P.

2000US-0190076P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGTTTCATGACG 135
                                                                                                                                                                                                                                                                                                                                       9.83e-32
45.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                           12.61%
                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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17-MAR-2000;
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PR 18-APR-2000; 2000US-0199122P.
PR 71-WX-2000; 2000US-0215467P.
PR 72-WX-2000; 2000US-0215467P.
PR 77-WX-2000; 2000US-02154647P.
PR 77-WX-2000; 2000US-0211467P.
PR 11-WX-2000; 2000US-0211467P.
PR 14-AXIC-2000; 2000US-02254P.
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PR 14-AXIC-2000; 2000US-02344P.
PR 14-SEP-2000; 2000US-02344P.
PR 05-SEP-2000; 2000US-02344P.
PR 14-SEP-2000; 2000US-02349P.
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PR 14-SEP-2000; 200US-02349P.
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PR 14-SEP-2000; 2000US
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PR 20-CGT-2000; 2000GH-2047086P.
PR 20-CGT-2000; 2000GH-204708P.
PR 20-CGT-2000; 2000GH-2047108P.
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PR 2000GH-204418P.
PR 2000GH-204418P.
PR 2000GH-204418P.
PR 2
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W. Ϋ,

Patturajan M, Vernet CAM, Guo X, Boldog FL, Grosse I, Rothenberg ME, Ellerman I, I, Peyman J, Smithson G;

Gangolli EA, Burgess CE, Pa Tchernev VT, Miller CE, Gu JP, Gerlach V, Edinger S, I I J, Malyankar U, Millet I, Stone DJ,

Macdougall J,

Zhong M, (Taylor S, Alsobrook d Gunther E, 2002-590674/63.

P-PSDB; ABB98416

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isolated from a range of human tissues disclosed in the specification.
The nucleic acids, proteins, antibodies and (ant)agonists are useful in
the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
alegancies e.g. Addison's disease, allergies, autoimmune haemolytic
anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
cardiovascular disorders such as wiral, bacterial, fungal and epilepsy; and (f)
infections. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences
            $$$$$$$$$$$$$$$$$$$$
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Sequence 8899 BP; 1841 A; 2663 C; 2617 G; 1778 T; 0 U; 0 Other;

The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IGA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOVI4b is a prostasin-like protein, and the NOVI4b coding sequence localises to

NOVX polypeptides and encoding polynucleotides, useful for preventing or treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or

Claim 9; Page 99; 358pp; English.

pharmacogenomics.

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Human; NOV14b; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallerqic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiasthmatic; Newportective; Nootropic; Haptortorpoic; Newportective; Nootropic; Antibacterial; Virucide; Antiparastitic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IQA nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; prostasin-like protein; chromosome 16; gene; ds.
                                                                                                                                LeuValLeuProTrpLeuSerProHisSerLeuLeuGlyLeuTrpGlyPhe 357
                                                                                                                                                      747 CITGLETCECCEGGCECTCTCCCCACACTCTCTCGGGCCTCTGGGGGGTTT 697
               8899
117
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Mismatches:
               Length:
Matches:
                                                                 Indels:
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100.00%
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                                                                 4.768
                                     Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                                                                  341
                                                                                                                                                                                                                                          ABN85393;
                                                                 Query Match:
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Human; NOV14a; cytostatic; Cardiant; Antiinflammatory; Immunosuppressive; Antiallergic; Haemostatic; Anti-HIV; Antidiabetic; Anorectic; Antiasthmatic; Nephrotropic; Hepatotropic; Neuroprotective; Nootropic; Antibacterial; Virucide; Antiparasitic; Relaxant; Anticonvulsant; Gene Therapy; NOV; cancer; heart disease; inflammation; autoimmune disorder; allergy; blood disorder; AIDS; diabetes; obesity; asthma; IgA nephropathy; cirrhosis, arthritis; Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy; wasting disorder; prostasin-like protein; chromosome 16p11.2; gene; ds.
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Location/Qualifiers

product= "NOV14b"

WO200255704-A2

18-JUL-2002

1. .1161 /*tag= 8

Spytek KA;

Shenoy S,

Casman SJ,

Li L, Zerhusen BD,

Padigaru M,

(CURA-) CURAGEN CORP.

18-APR-2001; 28-FEB-2001; 09-MAR-2001;

2001US-0260417P. 2001US-0260831P. 2001US-0272338P.

09-JAN-2001; 10-JAN-2001;

2001US-0274876P 2001US-0284704P

09-JAN-2002; 2002WO-US000554.

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NOVX polypeptides and encoding polynucleotides, useful for preventing treating NOVX-associated disorders e.g. cancer, inflammation, or Alzheimer's disease, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                              Padigaru M, Li L, Zerhusen BD, Casman SJ, Shenoy S, Spytek KA, Zhong M, Gangolli EA, Burgess CE, Patturajan M, Vernet CAM; Taylor S, Tchernev VT, Miller CE, Guo X, Boldogo FL, Grosse WM, Alsobrook JP, Gerlach V, Edinger S, Rothenberg ME, Ellerman K, Macdougall J, Malyankar U, Millet I, Peyman J, Smithson G; Gunther E, Stone DJ;
                                                                                                                                                                                                                                                                                                                           Claim 9; Page 97-98; 358pp; English.
                               09-JAN-2001; 2001US-0260417P.
10-JAN-2001; 2001US-0260831P.
28-FEB-2001; 2001US-0272338P.
09-MAR-2001; 2001US-0284704P.
         09-JAN-2002; 2002WO-US000554.
                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                        WPI; 2002-590674/63.
P-PSDB; ABB98415.
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or

The present sequence is a coding sequence for a NOV protein. The NOV proteins and coding sequences are useful for treating or preventing NOV-associated disorders or in the manufacture of a medicament for treating the disorders, such as cancer, heart disease, inflammation, autoimmune disorders, allergies, blood disorders, AIDS, diabetes, obesity, asthma, IGA nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections (e.g. bacterial, viral, parasitic), stroke, muscular dystrophy, epilepsy, and other wasting disorders associated with chronic diseases. NOV14a is a prostasin-like protein, and the NOV14a coding sequence localises to chromosome 16pl1.2 Sequence 1726 BP; 284 A; 581 C; 499 G; 362 T; 0 U; 0 Other;

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Conservative:
Mismatches:
Indels:
Gaps: 9e-05 16.00 100.00% 100.00% 4.48% Best Local Similarity: Percent Similarity: Alignment Scores: Pred. No.: Query Match: Score:

US-10-037-417-46 (1-357) x ABN85392 (1-1726)

1 MetalaGlnLysGlyValLeuGlyProGlyGlnLeuGlyAlaValAla 16

Search completed: February 25, 2004, 22:21:32 Job time : 431 secs

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A1393068 L262509.x
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BB593614 BB593614
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A1623099 tu49f05.x
A1193435 qe58e10.x
CB116948 K-EST0161
AUZ98208 AUZ98208
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(without alignments)
4271.153 Million cell updates/sec
                                                                                                                        1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                - nucleic search, using frame plus p2n model
                                                                                                                                                                                                  27513289 segs, 14931090276 residues
                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                    Post-processing: Listing first 45 summaries
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Ygapop 60.0 , Ygapext e
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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285

199 165 219 105

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456 bp mRNA linear EST 28-OCT-1998 qd49f07.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1732837 3' similar to SW:MCP6_MOUSE P21845 MAST CELL PROTEASE 6 PRECURSOR ;, mRNA sequence.
                                           cececaerescentererecescentereces 345
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                                                                                            LeuAlaLeuLeuArgLeuAlaSerProAlaSerLeuGlyProAlaValTrpProValCys
                                                                                                                                                                                                160 LeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGly
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1414920-14179291,1520904-1522439); NCI CGAP GC4 pool 1 LLAM
1464920-14179291,1520904-1522439); NCI CGAP GC4 pool 1 LLAM
1557096-1258631,1469064-1470983, 1475592-1476743);
NCI CGAP Pr2 Dool 1 LLAM 2457-2459, 2758-2759, 3062-3068
(IMAGE CLONELDS 986608-986759,1101192-1101959,
1217928-1220615); NCI CGAP Col0 pool 1 LLAM 2644-2653,
1877-2872 (IMAGE CLONELDS
1057416-1061255,11445984-1145351). (10% of the driver population), plus a pool 0 3,840 arrayed clones from NCI CGAP Subl (IMAGE CloneIDS 271058616-2710535) and NCI CGAP Subl (IMAGE CloneIDS 271058616-2710535) and NCI CGAP Subl (IMAGE CloneIDS 271058616-2710535)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone=ITMAGE:2736337"
/lab_host="DRIOB (Life Technologies)"
/clone=ITMAGE:2736337"
/lab_host="DRIOB (Life Technologies)"
/clone=Ithe=NNI CGAP_Sub5"
/clone=Ithe=NNI CGAP_Sub5
/note="Vector: pit-1" Not I; Site 2: Eco RI; NCI CGAP_Sub5
is a subtracted library derived from NCI CGAP_Sub4. The
NCI CGAP_Sub5 library had 3 million recombinante. A
single-stranded DNA preparation of NCI CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising the IMAGE pool (IMAGE CloneIDs
1322376-1323911, 1456008-1456775,1500552-1502855);
NCI CGAP_Kid5 pool 1 LLAM 3338-3342,3722-3725, 3776-3778
(IMAGE CloneIDs 1323912-1325831, 1471368-1472903,
1462104-1493255); NCI CGAP_Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE CloneIDs
                                                                                              Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: NCI-CGAP clone distribution
information can be found through the I.M.A.G.E. Consortium/LIML at:
Seq primer: MI3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the driver population), plus a pool of 11,136 clones from driver population, plus a pool of 11,136 clones from driver population, plus a pool of 5,472 clones from NCI_CGAP_Sub4 (IMAGE CloneIDS 2712592-2728969) (10% of the driver population). Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537
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                                                                                                                                                                                                                                                                                                                                                                   1. .537
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
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154.00
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                                                   Tumor Gene Index
Unpublished (1997)
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AUTHORS
TITLE
                                                                           JOURNAL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 456)
                                                                           NCI-GGAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This Clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 712 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1732837"
                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="unknown"
                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                        1. .456
Homo sapiens
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405

120 ArgAlaValAlaAlaIleValValProAlaAsnTyrSerGlnValGluLeuGlyAlaAsp 139

100 GluTrpSerValLeuLeuGlyValHisSerGlnAspGlyProLeuAspGlyAlaHisThr 464 characticaracticaracticaracticaracticaracticaracticaractical

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ORIGIN

Score:

Query Match: DB:

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Pred. No.:

Alignment

DRIGIN

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/clone="CS0CAPOLYGIT"
/tissue type="THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa 735 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 721: 319 335 9256
Fax: 319 335 9565
Email: bento-soares@ulowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
                                                                                                                                                                                                                                                                                                                                                                                                     EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metacas; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 296)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                               253 GlyargrppheGlnalaGlyIleThrSerPheGlyPheGlyCySGlyArgArgAsnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 ProGlyValPheThralaValAlaThrTyrGluAlaTrp11eArgGluGlnValMetGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF561257
296 bp mRNA linear EST 12-DF
UI.R-CO-hh-h-07-0-UI.rI UI-R-CO Rattus norvegicus cDNA clone
UI-R-CO-th-h-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 SerGlubroGlyProAlaPheProThrGlnProGlnLysThrGlnSerAsp. 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
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Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                               930
57
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Conservative:
Mismatches:
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|strain="Spraque-Dawley"
|db_xref="taxon:10116"
|clone="Ul-R-CO-hh-h-07-0-Ul"
|dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
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97044477
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Location/Qualifiers
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BF561257.1 GI:11670987
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3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 GTCCAGGAGGCAGATCCTCTCCCTCTCCCTGGGTGCTACAGGAAGTGGAGCTAAGGCTG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 GlnIleLeuProGlyMetLeuCysAlaGlyTyrProGluGlyArgArgAspThrCysGln 240
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Li, W. Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact
Feng Liang Email: fliangolifetech.com URL:
http://full.length.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOCAP001AD09FM1.
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                                                                                                                                                                                                                                                                                                                                                                161 ProhrgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGlyTrpGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BMail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.;
more information about this cluster, see
                                                                        Length:
Matches:
Conservative;
Mismatches:
Indels:
                                                                                                                                                       Gaps:
                                                                                                                                                                                    US-10-037-417-46 (1-357) x AI190509 (1-456)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
                                                                  1.06e-103
128.00
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NbHL19W."
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                                                                                                 Percent Similarity:
Best Local Similarity:
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EST

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

source

FEATURES

24

RESULT 3
BX436299
LOCUS
DEFINITION

292

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Similarity:
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/lab_host="DH10B (Life Technologies)"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib="UT-R-CO"
/clone lib-ray derived from the UT-R-CO
polylinker; Site_l: Not I; Site_2: Ecc RI; The UT-R-CO
library is a subtracted library derived from the UI-R-CO
mixture of individually tagged normalized libraries
constructed from tat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, and muscle: The UT-R-EI
library consisted of a mixture of individually tagged
normalized libraries constructed from 8, 12 and 18-day
normalized libraries constructed from 8, 12 and 18-day
normalized libraries constructed from 8, 12 and 18-day
normalized libraries constructed from 8 a follows identification of the library of origin of a clone
allows identification of the library of origin of a clone
within the mixture. The subtracted library (UI-R-CO) was
constructed as follows: PCR amplified constructed to
been derived was used as a driver in a hybridization with
the pooled UI-R-AI and UI-R-EI clones from which 3' ESTS had
been derived was used as a driver in a hybridization of
single-stranded circles. The remaining single-stranded
circles (subtracted library) was purified by
hydroxyapatite column chromatcgraphy, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technologies) to generate the UI-R-CO
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA996811
UI-R-CO-hh-h-07-0-UI.S1 UI-R-CO Rattus norvegicus CDNA clone
UI-R-CO-hh-h-07-0-UI.3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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375 Newton Road , 4156 MEBRF, Iowa City, IA 52242,
Tel: 319 335 8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 PCCCTCATCGCCCCTTCCTGGGTCCTCCGCTGCTCACTGTTTC 166
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Rattus norvegicus
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AA996811
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DRIGIN

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/clome="Ul-k-CU-nn-n-U'-Uul"
//dev stage="ddlt"
/lab host="Dtl10B (Life Technologies)"
/lab host="Dtl10B (Life Technologies)"
/clome_lib="Ul-R-CO"
/clome_lib="Vl-R-CO"
/clome_li
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Email: bento-scares@ulowa.edu
Oligo-dr track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
is likely internal to the message. and is also available
through Research Genetics This clone is also available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LINL (info@image.llnl.gov). IWAGE
ID=1781449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
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/clone="UI-R-C0-hh-h-07-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Sprague-Dawley"
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BY236668
BY236668.1 GI:26417846
EST.
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Let (Dazaki Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hune, D.A., Quackenbush, J., Schrimi, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dagaterland, T., Gartiohdi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincch, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Namata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sandelin, A., Schoeider, C., Semple, C.A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, X., Zhu, Yang, J., Yang, J., Yang, J., Mayazaki, A., Sasaki, D., Shizaki, R., Rawa, T., Fukuda, S., Hara, M., Hangaraki, M., Sasaki, D., Shizaki, K., Sasaki, J., Sasaki, J., Shizaki, Y., Shinayasa, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasunishi, A., Yasu
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 351)
Mus musculus (house mouse)
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Contact: Yoshihide Hayashizaki
Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
181: 81-45-503-922
Nature 420, 563-573 (2002)
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Fax: 0:1-30-20-30-30.16
Email: genome-res@gsc.riken.go.jp,
 Alzawa, X., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, X., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
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 Ohno, M., Sakai, K., Sakazume, N., Saaski, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared
 Human Genome Sequence Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
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 Encyclopedia Project of Genome Exploration Research Group in Riken
 Division of Experimental Animal Research in Riken contributed to

prepare mouse issues.

Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NB 68131 USA) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers

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Email: genome-tres@gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
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10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA
nonredundant cONA library. Genome Res. 11 (2), 281-289 (2001)
Charary was prepared and sequence clustering for construction of a cDNA library was prepared and sequence of in Mouse Genome
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Division of Experimental Animal Research in Riken contributed to
                                                                                                   Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Cmaha,NB 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, adult inner ear"
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Othar GSSs: RPCI-23-466N15.TJ RPCI-23-466N15.TV RPCI-23-466N15.TVB

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

The 1 191 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong, med. buffalo.edu). Clones may be purchased from

(pieter@dejong, med. buffalo.edu). Clones may be purchased from

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RPCI-23-466N15.TJB RPCI-23 Mus musculus genomic clone
AZ252377
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Dopublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchino-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
Email: genome-resegsc.riken.go.jp,
URL:http://genome-sesc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Dases 1 to 433)
1 (Lasas 1 to 433)
1 (Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatau,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,
Hayatau,N., Hiramoto,K., Hiraoka,T., Kodima,Y., Kodno,H., Kodad,M.,
Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,
Sagaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Tanaka,T., Tomaru,A., Togawa,A., Takahashi,F., Takaku-Akahira,S.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura,T., et al.
/ido_lib="RPCI-23"
//clone_lib="RPCI-23"
//oce="Organ: Kidney/Brain; Vector: pBACc3.6; Site_1:
EcoR1; Site_2: ECOR1; Female C57BL/6J mouse kidney and/or
brain genomic DRA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DRA was cloned into the pBACc3.6 vector at the
ECOR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Mus musculus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1. (Bases 1 to 454)

1. (Bases 1 to 454)

1. Sarber, M., Base, M., Rose, R., Barber, T., Duval, B., Hamil, C.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah Genome Center
University of Utah
Res. 300, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Shibata, K., Itoh, M., Carninci, P., Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA consciously construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ875648 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC2M0190113 F, genomic survey sequence.
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                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="F93010BE12"
/tissue_type="inner ear"
/dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: I column: 13
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Seq primer: CGTTRAAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 454.
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1. .433
/organism="Mus musculus"
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Fax: 801 585 7177
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                                                                                                                                                                                                      e mouse tissues.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinaes. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gil 4732114/gbl AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIII0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

I (Dases I to 433)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayateu,N., Hiramoto,F., Hiraoka,T., Hirozane,T., Imotani,K.,

Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,

Okazaki,Y., Okido,T., Salto,R., Sakai,C., Sakai,K., Sakazume,N.,

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Sagabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Bncyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB850564 EST 26-NOV-2001
BB850564 RIKEN full-length enriched, adult inner ear Mus musculus
cDNA clone F930108A18 5', mRNA sequence.
BB850564
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/lab host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clome lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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'organism="Mus musculus"
                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
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Smail: cgapbs-r@mail.nih.gov
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                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-1: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. (10), 1757-171 (2000)

Sugahara,Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a provedopedia: real-time sequence clustering for construction of a please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                   Email: genome resigns.riken.go.jp,

TRI.http://genome.gsc.riken.go.jp,

Carninci.p. Shibata,Y. Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Matshuki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

and Hayashizaki,Y.

Patram, Inoue,Y., Kira,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGENCOURT_7906304 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6140519 BU164841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
/clone_lib="RIKEN full-length enriched, adult inner ear"
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I. (baese 1 to 875)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e mouse tissues.
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JOURNAL
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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                    COMMENT
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1..875
| organism="Homo sapiens"
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| mol_type="mgNn" |
| db_xref="taxon:966" |
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| tissue_type="retinoblastoma" |
| lab_host="DH10B (phage-resistant)" |
| clone=lib="NH1MGC 67" |
| note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 22-MAY-2003
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-remail.nh.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
http://image.llnl.gov
Plate: NDAM447 row: j column: 12
Plate: NDAM447 row: j column: 12
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NIH-WGC http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: The I.M.A.G.B. Consortium

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information

Clone distribution: MGC clone distribution information

Clone distribution on the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI3459 row: d column: 24

High quality sequence stop: 645.
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CD251990
CD251990.1 GI:31012456
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Mismatches:
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Location/Qualifiers
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/tlssue_type="adenocarcinoma, cell line"
/tlssue_type="adenocarcinoma, cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 16-0CT-2002
               /clone="IMAGE:30383555"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances) "
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances) "
/clone lib="NIH MGC 180"
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Site 2: EcoNv (destroyed); Library is oligo-dT primed and directionally cloned (EcoNv site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM2897 row: n column: 15
High quality sequence stop: 423.
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BUBG0221
AGENCOURT 10435504 NIH_MGC_107 Homo mapiens cDNA clone INAGE: 6651279 5', mRNA sequence.
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Matches:
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db xref="taxon:9606"
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AUTHORS
TITLE
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Alignment Scores:

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Search completed: February 26, 2004, 00:06:29 Job time : 2502 secs Sequence 109, App Sequence 109, App Sequence 109, App Sequence 109, App Sequence 109, App

1, Appli 10, Appl 1, Appli 5, Appli

Sequence

Word size:

Sequence:

Run on:

Sequence 1, 1 Sequence 10,

Sequence Sequence Sequence

Appli Appli Appli Appli Appli Appli Appli Appli

Sequence

Sequence Sequence

Sequence

60, Appl 2, Appli 3, Appli 7, Appli 44, Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 7

Sequence 44, Sequence 46, Sequence 58,

Sequence

Patent No. 522 Sequence 22,

122, App 122, App 19, App1 122, App 122, App

Sequence

Patent No.

Sequence

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US-09-280-116-72/c
Sequence 72, Application US/09280116A
Patent No. 6331427
GENERAL INFORMATION:
TETLICANT: Robison, Keith E.
FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION UNMER: US/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOPTHARE: PatentIn Ver. 2.0
SSOTHARE: PatentIn Ver. 2.0
LENGTH: 506
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Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: n = a,
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LOCATION: (1)...(506)
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TYPE: DNA
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1, Appli
19, Appli
9, Appli
72, Appli
6, Appli
6, Appli
28, Appli
122, Appl
                                                February 25, 2004, 18:59:12 ; Search time 97 Seconds (without alignments) 2042.448 Million cell updates/sec
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                                                                                          357
1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
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6: /cgn2 6/ptodata/2/ina/btcttls comB.seq:*
   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                  nucleic search, using frame_plus_p2n model
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US-09-244-111-3
US-09-070-526-1
US-09-008-271A-19
US-09-386-642-9
US-09-618-259-72
US-09-618-259-6
US-09-280-116-28
US-09-280-116-29
US-09-280-116-29
US-09-80-116-29
US-08-906-616-122
US-08-906-616-122
                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                 682709 seqs, 277475446 residues
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60.0
7.0
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                                                                                                                          60.0 , Xgapext 6
60.0 , Ygapext 6
6.0 , Fgapext
6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length
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792
944
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TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
FILE REFERENCE: P7391
CURRENT APPLICATION NUMBER: US/09/244,111
CURRENT APPLICATION NUMBER: 00/073,961
EARLIER APPLICATION NUMBER: 60/073,961
EARLIER APPLICATION NUMBER: 00/073,961
SARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
LENGTH: 792
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329 TGCCAGGGTGATTCCGGAGGCCCGCTGGTGTGTGAGGAA 291
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ZIP: 19482
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,526
971.1NG DATE: 30-APR-1998
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Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6100059
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCUTTAN, CHRISTOPHER
APPLICANT: CLINKENBEARD, HELEN
APPLICANT: BURGESS, NICOLA
ITITLE OF INVENTION: No. 6100059el Compounds
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER: GB 9711952.3
APPLICATION NUMBER: GB 97309646.4
FILING DATE: 9-0777
APPLICATION NUMBER: EP 97309646.4
FILING DATE: 1-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAMME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
                                                                           Sequence 3, Application US/09244111
Patent No. 6566498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: RAINER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
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100.00%
100.00%
3.64%
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (85)..(708)
US-09-244-111-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                      GENERAL INFORMATION:
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                                                            US-09-244-111-3
                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/008,271A
FILING DATE: 16-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: «UNKNOWN»
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
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APPLICANT: Bandman, Jennifer L.
Yue, Henry
Guegler, Karl J.
Corley, Neil C.
Tang, Tom Y.
Shah, Purvi
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-037-417-46 (1-357) x US-09-070-526-1 (1-944)
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REGISTRATION NUMBER: 41,201
REFERENCE/DOCKGT NUMBER: PF-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09008271A Patent No. 6203979 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
REFERENCE/DOCKGT NUMBER: G
TELECOMUNICATION INFORMATION
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 19
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100.00%
100.00%
3.64%
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ZIP: 94304
COMPUTER READABLE FORM:
                                                   TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 944 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                0.00149
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Best Local Similarity:
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DB:
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OTHER INFORMATION: Description of Artificial Sequence: Fusion gene OTHER INFORMATION: with homo sapien serine protease catalytic domain
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; Sequence 72, Application US/09618259
; Patent No. 6642013
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: No. 6442013el Extracellular Serine Protease; FILE REFERENCE: D6020C192
; CURRENT APPLICATION NUMBER: US/09/618,259
; CURRENT FILING DATE: 2000-07-18
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 72
; NUMBER OF SEQ ID NOS: 72
; LENGTH: 1343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1049
113
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                                                                                                                           994
0 0 0 0
                                                                                                                                                                                                                                                                                                                  770 GACACGTGCCAGGCGATTCTGGAGGCCCCCTGGTGTGT 808
                                                                                                                                                                                                                                                                                              237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys
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Matches:
Conservative:
Mismatches:
                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                           US-10-037-417-46 (1-357) x US-09-008-271A-19 (1-994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Darrow, Andrew
APPLICANT: Qi, Jenson
APPLICANT: Qi, Jenson
TITLE OF INVENTION: Zymogen Activation System
FILE REFERENCE: ORT-1028
CURRENT FILING NUMBER: US/09/386,642
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-037-417-46 (1-357) x US-09-386-642-9 (1-1049)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                                                                                                                                                                   Indels:
               LIBRARY: COLNNOT27
CLONE: 1798496
SEQUENCE DESCRIPTION: SEQ ID NO: 19
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09386642
Patent No. 6420157
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                            100.00%
100.00%
3.64%
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IMMEDIATE SOURCE:
                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                     US-09-008-271A-19
                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-386-642-9
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Query Match:
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DB:
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APPLICANT: STROUPE, STEVEN D.
TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Nucleotide sequence encoding Tumor Antigen Derived OTHER INFORMATION: Gene-14 (TADG-14) protein; nt 1344-1360 NCBI accession OTHER INFORMATION: #AA343629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Underwood, Lowell J.
TITLE OF INVENTION: No. 6642013el Extracellular Serine Protease
FILE REFERENCE: D6020CIPP.
CURRENT APPLICATION NUMBER: US/09/618,259
CURRENT FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
                                                                                                                                                                                                                                                                                                                                        237 AspThrCysGlnGlyAspSerGlyGlyProLeuValCys 249
                                                                                                                                                                                                                                                                                                                                                                          213 GACACGIGCCAGGGCGATTCTGGAGGCCCCCTGGTGTGT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                         FEATURE:
; OTHER INFORMATION: Anti-sense sequence of TADG-14
US-09-618-259-72
                                                                                                                                                                                                                                                                                              US-10-037-417-46 (1-357) x US-09-618-259-72 (1-1343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-037-417-46 (1-357) x US-09-618-259-6 (1-1360)
                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: US 09/127,444
PRIOR FILING DATE: 1998-08-21
NUMBER OF SEQ ID NOS: .72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: FRIEDMAN, BAULA N.
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: KLASS, MCHAEL R.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEWART, KENT D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/09618259 ; Patent No. 6642013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-944-483-5; Sequence 5, Application US/08944483; Patent No. 6232456
TYPE: DNA
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STROUPE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: COHEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                 Query Match:
DB:
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                                                                                                                                                     . No. :
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US-09-280-116-29/c

US-09-280-116-29/c

Sequence 29, Application US/09280116A

Sequence 29, Application US/09280116A

Sequence 29, Application

Sequence 29, Application

Sequence 29, Application

Sequence 29, Application

Sequence 29, Application

TITIE OF INVENTION:

TITIE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs

TITIE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs

TITIE REFERENCE: S800-24, 035800/176965

CURRENT FILING DATE: 1999-03-26

NUMBER OF SEQ ID NOS: 268

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 29

LENGTH: 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J.
APPLICANT: Gaines, Patrick J.
APPLICANT: Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 1990
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340
111
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Conservative:
Mismatches:
                  Conservative:
Mismatches:
Indels:
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                                                                                                                                                                            250 CAGGGAGATTCTGGGGGGCCCCTGGTCTGTGAA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 GlnGlyAspSerGlyGlyProLeuValCysGlu 250
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                                                                                                                  US-10-037-417-46 (1-357) x US-09-280-116-28 (1-340)
                                                                                                                                                      240 GlnGlyAspSerGlyGlyProLeuValCysGlu 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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; Sequence 122, Application US/08906769
; Settl No. 6077687
; GENERAL INFORMATION:
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11.00
100.00%
100.00%
3.08%
  11.00
100.00%
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3.08%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
                Percent Similarity:
Best Local Similarity:
Query Match:
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No.:
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TITLE OF INVENTION: Mucleic Acid Molecules Encoding Human Protease Homologs FILE REFERENCE: 5800-24, 035800/176965
CURRENT APPLICATION NUMBER: U$/09/280,116A
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 268
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 340
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: trypsin-like serine proteases
US-09-280-116-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 CysGlnGlyAspSerGlyGlyProLeuValCys 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-037-417-46 (1-357) x US-08-944-483-5 (1-262)
                                                                                                                                                                                          MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPANE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILLING DATE: US/08/944,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
TITLE OF INVENTION: OF THE PROSTATE NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abbott Park CITY: Abbott Park CITY: Abbott Park COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6183.US.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 28, Application US/09280116A Patent No. 6331427 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELERAX: 847/938-2623
TELEX.
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-280-116-28/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
US-08-944-483-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
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/note= "At pos. bp 301, change A to W; at pos. bp 397, change C to W; at pos. bp 342, change C to Y; at pos. bp 331, change G to S. At pos. aa 100, 114 and 144, substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 122, Application US/08639075A

Sequence 122, Application US/08639075A

Patent No. 6150125

GENERAL INPORMATION:

APPLICANT: Grieve, Robert B.

APPLICANT: Rushlow, Keith E.

APPLICANT: Frank, Glann R.

APPLICANT: Stieglar, Gary

APPLICANT: Stieglar, Gary

APPLICANT: Gaines, Patrick J.

APPLICANT: Gaines, Patrick J.

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APPLICANT: Gaines, Patrick J.

APPLICANT: Gaines, Patrick J.

APPLICANT: Gain
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COMPUTER READABLE FORM:

MEDIUM TYPE Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CORRENT BAPELICATION NUMBER: US/08/639,075A

FILING DATE: 24-ARR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: COMPAIL, GATY J.

REGISTRATION NUMBER: 32,020

REFERENCE/DOCKET NUMBER: 2618-25-C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436
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Mismatches:
Indels:
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CLASSIFICATION: 536
ATTOWNEY/ABENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/EDOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
INFORMATION FOR SEQ ID NO: 122: SEQUENCE CHARACTERISTICS:
LEMOTH: 436 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNES: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.00
100.00%
100.00%
3.08%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA FRATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colorado
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Query Match:
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CITY: Denver
STATE: Colorad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-08-639-075A-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "At pos. bp 301, change A to
W; at pos. bp 342, change C to Y; at pos. bp 397, change C to
at pos. bp 431, change G to S. At pos. aa 100, 114 and 144,
substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Keith E.
APPLICANT: Rushlow, Shirley
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Gary
APPLICANT: Silver, Silver, Silver, Suite 3500
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STATE: Colorado
COUNTY: Denver
STATE: Colorado
COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-037-417-46 (1-357) x US-08-906-769-122 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GACACTTGCCAGGGAGATTCAGGTGGGCCATTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 AspThrCysGlnGlyAspSerGlyGlyProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
Indels:
                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 24-APR-196
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GATY J. 0.20
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEFONE: (303) 863-9700
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US/08/906,616
05-AUG-1997
      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 122, Application US/08906616
Patent No. 6121035
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.00
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3.08%
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LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
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Best Local Similarity:
Query Match:
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incorporation: 2..436

COTHER INFORMATION: /note= "At pos. bp 301, change A to other interpretation: /note= "At pos. bp 342, change C to Y; at pos. bp 337, change C to Y; at pos. bp 431, change G to S. At pos. as 100, 114 and 144, substitute Xaa."

SEQUENCE DESCRIPTION: SEQ ID NO: 122:
US-09-012-431-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09032215
Patent No. 6204010
GENERAL INFORMATION
FARE APPLICANT: Stiegler, Gary L.
APPLICANT: Gaines, Patrick J.
ITILE OF INVENTION: FIER PROTEASE PROTEINS, NUCLEIC
ITILE OF INVENTION: FIER PROTEASE PROTEINS, THEREOF
ITILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-037-417-46 (1-357) x US-09-012-431-122 (1-436)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 AspThrCysGlnGlyAspSerGlyGlyProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         257 GACACTTGCCAGGGAGATTCAGGTGGGCCATTG 289
                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
FILING DATE: 27-FEB-1998
CLASSIFICATION S36
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNAY'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
TELEFAX: (303) 863-0223
               INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 436 mucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                  11.00
100.00%
100.00%
3.08%
                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1700 Lincoln S
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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US-09-032-215-19
                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                        /note= "At pos. bp 301, change A to
W; at pos. bp 342, change C to Y; at pos. bp 397, change C to
at pos. bp 431, change G to S. At pos. aa 100, 114 and 144,
substitute Xaa."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDERS:
ADDRESSE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: USA
CONFUTER: RADBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tab PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 23-Jan-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                      436
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 AspThrCysGlnGlyAspSerGlyGlyProLeu 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 GACACTIGCCAGGGAGATICAGGIGGGCCATIG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
Stiegler, Gary
Gaines, Patrick J.
Silver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 122, Application US/09012431; Patent No. 6180383; GENERAL INFORMATION:
  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 190
                   TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-023
INPORATION FOR SEC ID NO: 122
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    0.0669
11.00
100.00%
100.00%
                                                                                                      LENGTH: 436 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                LOCATION: 2..436
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                       JS-08-639-075A-122
                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-012-431-122
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436
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                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Gaps:
                                                                                                                                                        US-10-037-417-46 (1-357) x US-09-032-215-19 (1-436)
                                                                                                        Score: 0.0669
Score: 11.00
Percent Similarity: 100.008
Best Local Similarity: 100.008
Ouery Match: 3.088
DB:
Alignment Scores:
Pred. No.:
Score:
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Search completed: February 26, 2004, 00:08:19 Job time : 101 secs

protein

Run on:

Sequence:

Perfect

Word size:

Searched:

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Sequence 612, App Sequence 612, App Sequence 194, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394, App Sequence 394
                     Sequence 10, Appl
Sequence 21306, A
Sequence 7606, App
Sequence 31, Appl
Sequence 29, Appl
Sequence 214, Appl
Sequence 2214, Appl
Sequence 261, Appl
Sequence 261, Appl
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Sequence 31, Appl
                     US-10-221-097-10
US-10-221-097-10
US-10-029-386-7606
US-10-042-865-31
US-10-042-865-29
US-10-176-847-85
US-09-980-107-2214
US-09-967-768A-141
                                                                                                                                                                                                                                                                                                                                 APPLICANT: WHYTE, DAVID
APPLICANT: CARNEPEBL, SEAN
APPLICANT: CARNEPEBL, SEAN
APPLICANT: CARNEPEBL, SEAN
APPLICANT: CARNEPEBL, SEAN
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVANTION: NOVEL PROTEASES
TITLE REPERBNCE: 038602/1214
CURRENT FILING DATE: 2001-06-26
CURRENT FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 52
LENGTH: 2457
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Patent No. US20020064856A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PLOWMAN, GREGORY
TYPE: DNA ORGANISM: Homo sapiens
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-MODEL=frame+ p.D.:.model -DEV=xlp
-MODEL=frame+ p.D.:.model -DEV=xlp
-MODEL=frame+ p.D.:.model -DEV=xlp
-Q=/CQ=1/USPTO spool p/US10037417/runat_24022004_101110_18195/app_query.fasta_1.519
-D=Published Applications NA -OFMT=fastap -SUFFIX=olip2n.rnpb -MINMATCH=0.1
-LOOPCI=0 -LOOPEXT=0 -UNITS=bits -STRRT=1 -END=-1 -MATRIX=oligo
-IRANS-humantq-0.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINENE=0
-MAXIEN=200000000 -USER=US10037417 @CGN 1 1.107 @runat_24022004_101110_18195
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY NEG SCORES=0 -MINIENE=0
-LONGLOG -DEV TIMEOUT=12 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-RGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                          February 25, 2004, 23:28:21 ; Search time 399 Seconds
(without alignments)
3133.050 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQKGVLGPGQLGAVANSDS.....TKSLVLPWLSPHSLLGLWGF 357
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| cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT NTW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
                                       GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Notal number of hits satisfying chosen parameters:
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                              score:
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Database :

US-09-888-615-52

Description

Score

No.

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258 AlaGlyIleThrSerPheGlyPheGlyCysGlyArgArgAsnArgProGlyValPheThr 277
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                                                                                                                                      TGGCCTTGGCAAGTGAGCTGCACCATGGAGGTGGCCACATCTGCGGGGGCTCCCTCATC 231
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                                                                                                                                                                                            TrpProTrpGlnValSerLeuHisHisGlyGlyGlyHisIleCysGlyGlySerLeuIle 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             772 GCAGGAATCACCAGCTTTGGCTTTGGCTGTGGAGAAACCGCCCTGGAGTTTTCACT
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                                                                                                                                                                                                                                                                                                                                    292 GCGGCCGAGTGGTCGGTACTGCTGGGCGTGCACTCCCAGGACGGGCCCCTGGACGGCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValCysLeuProArgAlaSerHisArgPheValHisGlyThrAlaCysTrpAlaThrGly
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                                    Conservative:
Mismatches:
Indels:
                                                                                                              US-10-037-417-46 (1-357) x US-09-888-615-52 (1-2457)
            Length:
Matches:
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US-10-221-097-10
; Sequence 10, Application US/10221097
; Publication No. US20030144476A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
          1.57e-260
272.00
100.00%
100.00%
76.19%
                               Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
Pred. No.:
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Sequence 21306, Application US/10029386
; Sequence 21306, Application US/10029386
; Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: AEOMICA-X-2
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21306
LENGTH: 315
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OTHER INFORMATION: MAP TO CHRI6.3
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.9
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Matches:
Conservative:
Mismatches:
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APPLICANT: Rizvi, Safia K.
APPLICANT: Rizvi, Safia K.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: Smith, Randall F.
APPLICANT: School School Computer Specific Computer Specific Computer Specific Specific Computer APPLICATION WOMBER: US/10/221,097 CURRENT APPLICATION WOMBER: DCT/USO1/07143 PRIOR FILING DATE: 2001-03-05 PRIOR FILING DATE: 2001-03-05 PRIOR FILING DATE: 2000-03-06 PRIOR FILING DATE: 2000-03-06 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIO
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US-10-221-097-10
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APPLICANT: Stone, David
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 2140-2-537
CURRENT APPLICATION NUMBER: US/10/042,865
CURRENT FILING DATE: 2002-05-17
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Mismatches:
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PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-10
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/274,876
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 264
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                                                                                                                                                                                                                                                                                    Guo, Xiaojia
Boldog, Ference I
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie I
Edinger, Shlomit R
Rothenberg, Mark E
Ellerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
                                                      Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
Zhong, Mei '
Gangolli, Esha A
Burgess, Catherine E
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APPLICANT: Li, Li
APPLICANT: Zerhusen, Bryan D
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Miller, Charles E
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Taylor, Sarah
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Gunther, Erik
                                     Zerhusen, Bryan D
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SEQ ID NO 31
LENGTH: 1161
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ORGANISM: Homo sapiens
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US-10-029-386-7606/c

US-10-029-386-7606/c

US-10-029-386-7606/c

Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CILE REFERENCE: ACID NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SEQ ID NO 7606

LENGTH: 543
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COTHER INFORMATION: MAP TO CHRIG.3
COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
COTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.1
COTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.3
COTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 4.3
COTHER INFORMATION: EXPRESSED IN BONE MARNOW, SIGNAL = 4.9
COTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
COTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
COTHER INFORMATION: STREAM HIT: AU142128-1, EVALUE 7.000-04
COTHER INFORMATION: NT HIT: U33446.1, EVALUE 0.000+00
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; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.6
; OTHER INFORMATION: NT HIT: G114779472, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q16651, EVALUE 1.00e-08
; OTHER INFORMATION: EST_HUMAN HIT: AU142128.1, EVALUE 0.00e+00
US-10-029-386-21306
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Publication No. US20040029216A1
GENERAL INFORMATION: Application Applicant: Padigaru, Muralidhara
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US-10-042-865-31
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US-09-948-094-1
US-09-948-094-1
Sequence 1, Application US/09948094
Sequence 1, Application US/09948094
Sequence 1, Application US2002009625A1
SEGUENCE 1. PROFESSE 1. Sequence 1. APPLICANT: The Brightm and Women's Hospital, Inc.
APPLICANT: Mok, Samuel
TITLE OF INVENTION: Methods of Detecting Cancer Based on Prostasin FILLE REPRESENCE: 81994/28243
FULLE REPRESENCE: 81994/28243
CURRENT APPLICATION NUMBER: US/09/948,094
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
FILE REPERENCE: 44921-5028-WO
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Matches:
CURRENT APPLICATION NUMBER: US/10/176,847 CURRENT FILING DATE: 2002-06-21 NUMBER OF SEQ ID NOS: 112 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 85 LENGTH: 1733
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SOFTWARE: Patentin version 3.0
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LOCATION: (229)..(1260)
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                                                                                                                                                                                                 TYPE: DNA; ORGANISM: Homo sapiens
US-10-176-847-85
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Publication No. US20030068636A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
TITLE OF INVENTION:
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TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: David

TITLE OF INVENTION: David

TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-537
CURRENT APPLICATION NUMBER: US/10/42,865
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/260,417
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-02-28
PRIOR PEDICATION NUMBER: 60/24,876
PRIOR FILING DATE: 2001-04-08
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
SOFTWARE: PARENTE: ALGORITH NUMBER: 60/284,704
SOFTWARE: PATENTING NUMBER: 60/284,704
SOFTWARE: PATENTING DATE: 2001-04-18
INUMBER OF SEQ ID NOS: 264
SOFTWARE: PATENTING NUMBER: 60/284,704
PRIOR FILING DATE: 2001-04-18
ILENGTH: 1726
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Matches:
Conservative:
Mismatches:
Indels:
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Burgess, Catherine E
Patturajan, Meera
Vernet, Corine A.M
Taylor, Sarah
                                                                                                                                                                                                                                                                                                              Tcherney, Velizar T
Miller, Charles E
Guo, Xiaojia
Boldog, Ference L
Grosse, William M
Alsobrook II, John P
Gerlach, Valerie L
Edinger, Shlomit R
Rothenberg, Mark E
Bllerman, Karen
MacDougall, John
Malyankar, Uriel M
Millet, Isabelle
Peyman, John
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Gunther, Erik
                       Casman, Stacie J
Shenoy, Suresh G
Spytek, Kimberly
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CRGANISM: Homo sapiens
US-10-042-865-29
                                                                                                                   Zhong, Mei
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Best Local Similarity:
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Pred. No.:
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Query Match:

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AFFILCANT: AGIEN CLAIL

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT PAPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/225,149
PRIOR APPLICATION NUMBER: 60/225,149
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
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US-10-101-510-447

Sequence 447, Application US/10101510

Publication No. US20030148295A1

GENERAL INFORMATION:

APPLICANT: WANG, VIXIN

TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012

CURRENT FILING DATE: 2002-03-20

PRIOR APPLICATION NUMBER: 60/276,947

PRIOR FILING DATE: 2001-03-20

WUMBER OF SEQ ID NOS: 805

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 447
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John MONAHAN
Manjula GANNANARAPU
Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Robert C. BAST, Jr.
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Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-10-097-340-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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LENGTH: 1834
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| Sequence 14.1. Application US/09967768A
| Patent No. US20020150877A1
| GENERAL INFORMATION:
| APPLICANT: Augustus, Meena
| TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
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| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| FILE REFREENCE: 689220-72
| CURRENT APPLICATION NUMBER: US/60/236,034
| PRIOR FILING DATE: 2000-09-28
| PRIOR FILING DATE: 2000-09-28
| PRIOR FILING DATE: 2000-09-28
| PRIOR FILING DATE: 2000-09-28
| PRIOR FILING DATE: 2000-09-28
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Matches:
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Matches:
Conservative:
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     CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2214
LENGTH: 1834
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; ORGANISM: Homo sapiens
US-09-967-768A-141
                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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US-10-097-340-261
                                                                                                                                                                                                                                                                                                                                                                                         US-09-880-107-2214
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Sequence 3, Application US/10325745;
Sequence 3, Application US/10325745;
Publication No. US203030135028A1
GENERAL INFORMATION:
TITLE OF INVENTION: Human Serine Protease and Serpin Polypeptides
FILE REFERENCE: PF391D1
CURRENT APPLICATION WHEER: US/10/325,745
CURRENT APPLICATION NUMBER: US 09/244,111
PRIOR APPLICATION NUMBER: US 09/244,111
PRIOR APPLICATION NUMBER: US 60/073,961
PRIOR FILING DATE: 1999-02-06
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 792
                                                                                                                                                                                                                             RESULT 14
US-10-101-510-621
Sequence 621, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
TITLE OF INVENTION: EXPRESSION PROFILES AND FILE OF UNDER 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT PILING DATE: 2002-03-20
PRIOR FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 805
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Matches:
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Matches:
Conservative:
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NAME/KEY: CDS

LOCATION: (85) .. (708)

OTHER INFORMATION:
US-10-325-745-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
; LENGTH: 3382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-447
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Pred. No.:
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Sequence 612, Application US/10101510
; Sequence 612, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
    APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
    FILE REFERENCE: 15117.0012
; CURRENT PAPLICATION NUMBER: 00/276,947
; PRIOR PEPLICATION NUMBER: 60/276,947
; PRIOR PEPLICATION NUMBER: 60/276,947
; PRIOR PEPLICATION NUMBER: 60/276,947
; RIGHT SPELICATION NUMBER: 60/276,947
; RIGHT SPELICATION NUMBER: 00/276,947
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Matches:
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Job time : 406 secs
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; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 621; LENGTH: 988; TENGTH: 988; TYPE: DNA ORGANISM: Homo sapiens US-10-101-510-621
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US-10-101-510-612
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/clone lih="Spitheline poly (A+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped with tabacco acid pyrophosphatase (TAP) and then decapped with tabacca acid pyrophosphatase (TAP). The decapped with tabacca ware ligated and the first including Sfil site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using Sfil cloned into DraIII- digested pwm185-Fil3 vector. The cloned into DraIII- digested pwm185-Fil3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coll Top10F' by electroporation method. The CDNA libraries constructed by this method are full-length enriched cDNA library."
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1. (bases 1 to 318)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)
                                                                                                                                                                                                            318 bp mRNA linear EST 06-MAR-2002
K-ESTO101694 S9SNU601 Homo sapiens cDNA clone S9SNU601-51-E07 5',
mRNA sequence.
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100.0%; Pred. No. 1.9e-20;
Live 0; Mismatches 0;
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

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| organism="Momo sapiens"
| organism="Momo sapiens"
| mol_type="mRNA"|
| db xref="taxon:9606" |
| clone="INAGE:2109831" |
| tissue_type="B-cell, chronic lymphotic leukemia" |
| tissue_type="B-cell, chronic lymphotic leukemia" |
| lab_host="UBIOB" |
| lab_host="UBIOB" |
| lab_host="TINIOB" |
| lab_host="Nor I SiTe I: Nor I: SiTe 2: Eco RI; lst strand cDNA polylinker; Site I: Nor I: Site 2: Eco RI; lst strand cDNA polylinker; Site I: Nor I: oligo[dr) primer [5/ was primed with a Nor I - oligo[dr) primer [5/ was primed with a Nor I - oligo[dr) primer [5/ was primed with a Nor I - oligo[dr) primer [5/ was primed primed with a Nor I - oligo[dr) primer [5/ was primed primed with a Nor I - oligo[dr) primer [5/ was primed primed with a Nor I - oligo[dr) primer [5/ was primed primed with a Nor I - oligo[dr) primer [5/ was primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed primed pri
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A1393077 360 bp mENA linear EST 30-MAR-1999 eQS5£08.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109831 3' similar to SW:PSSS HUMAN Q16651 PROSTASIN PRECURSOR ; mRNA
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Best Local Similarity. 100.0%; Pred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0; Indels
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nammails; butneria; Frimates; Catarrini; Hominidae; Homo.

1 (bases 1 to 294)

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldher, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Barle-Hughes, J., Fine, L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Jr.,

Kalley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nquyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Bednarik, D.E., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, B.J.,

Inmke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melson, P., Kim, A.K.,

Baymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                      EST 18-APR-1997
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9712 Medical Center Drive, Rockville, MD 20850 USA
19712 Medical Center Drive, Rockville, MD 20850 USA
19713 3018659423
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Uterus tumor I"
/note="Organ: uterus, Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                  AA300017 294 bp mRNA linear EST 18-2
EST12620 Uterus tumor I Homo sapiens cDNA 5' end similar to
prostasin, mRNA sequence.
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6.1%; Score 67; DB 9; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e-20;
Matches 67; Conservative 0; Mismatches 0; Indels
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/db_xref="ARTO" (inhost):108171"
/db_xref="taxon:9606"
/deV_stage="adult"
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Bioinformatics
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226 AAGACCCAGTCAGAT 240
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BX436299 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP001YG17
3-PRIME, mRNA sequence.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7995.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP001AD09FM1&cluster=7995.f. Contact
From Liang Email : fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001AD09FM1.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 1.4e-52;
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sapiens

Homo

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

BX436299

ACCESSION

VERSION KEYWORDS

DEFINITION

RESULT 3 BX436299

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Matches 135;

Query Match

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